

Access DB# 49312

SEARCH REQUEST FORM
Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>8/20/01</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>8/21/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>03</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2001, 21:25:24 ; Search time 1076.8 Seconds
(without alignments)
7325.921 Million cell updates/sec

Title: US-09-461-646-1_COPY_667_1176

Perfect score: 510

Sequence: 1 gcggctaccgactggaaga.....agatgtacggagacatggca 510

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: gb_ba2.*
- 3: gb_ba3.*
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- 5: gb_in2.*
- 6: gb_in3.*
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- 9: gb_pat1.*
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- 12: gb_pl1.*
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- 95: gb_ro2.*
- 96: gb_in4.*
- 97: gb_pr10.*
- 98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	510	100.0	1900	97	HSU14750
2	510	100.0	2075	9	AR018957
3	510	100.0	2075	10	I11636
4	510	100.0	2075	10	I32210
5	510	100.0	2075	97	HUMCONRO
6	510	100.0	2312	93	HSCTGF
7	451.4	88.5	1598	7	U70060
8	451.4	88.5	2330	7	BTAF000137

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I11636	Sequence	1
I32210	Sequence	1
M92934	Human	conne
X78947	H.sapiens	m
U70060	Sus	scrofa
AF000137	Bos	tauru

us-09-461-646-1_copy_667_1176.rge

Tue Aug 21 08:16:51 2001

AUTHORS Sutter, T.R.
 TITLE Direct Submission
 JOURNAL Submitted (16-SEP-1994) Thomas R. Sutter, Toxicological Sciences, Hygiene 7032, Johns Hopkins University, 615 North Wolfe Street, Baltimore, MD 21205, USA

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CDS
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 M92934 and M36965"
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 BASE COUNT 513 a 420 c 462 g 505 t
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 Best Local Similarity 100.0%; Pred. No. 6.4e-131;
 Matches 510; Conservative 0; Indels 0; Gaps 0;

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 QY 61 ctggtccagaccagagtagtgagcctgttccaagacctgtggatgggcatctccacc 120
 Db 378 CTGTGTCACAGACAGAGTGGAGCGCTGTTCACAGACCTGTGGATGGGCAATCTCCACC 437
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 QY 301 cgaactaaatctgtgagtagtaccgcagccgctgctacacccccacagaccacc 360
 Db 618 CGAGCTAATTTCTGTGGAGTATGTACCGAGCGCGGCGGATGCTGCACCAAGAACACC 677

U83916 Sus scrofa
 M70642 Mouse Fisp-
 M80263 Mouse mRNA
 AB023068 Rattus no
 AF120275 Rattus no
 AJ298335 Gallus ga
 AJ271167 Notophtha
 U43524 Xenopus lae
 AL354866 Human DNA
 AX034368 Sequence
 AX034367 Sequence
 AF079531 Rattus no
 AF309555 Bos tauru
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 U43523 Xenopus lae
 X96584 H. sapiens m
 U37063 Xenopus lae
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 BC001271 Homo sapi
 U62015 Homo sapien
 Y12084 H.sapiens m
 Z98053 Homo sapien
 Y11307 H.sapiens C
 AX035239 Sequence
 AB015877 Rattus no
 AF218568 Rattus no

ALIGNMENTS

RESULT 1
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 LOCUS Human connective tissue growth factor mRNA, partial cds.
 DEFINITION
 ACCESSION U14750
 VERSION U14750.1 GI:984955
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1900)
 AUTHORS Cody, C.W., Walker, N.J., Greenlee, W.F. and Sutter, T.R.
 TITLE Connective tissue growth factor mRNA is expressed in human
 keratinocytes as an immediate early gene that responds to serum,
 EGF, or wounding.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1900)
 AUTHORS Sutter, T.R., Guzman, K., Dold, K.M. and Greenlee, W.F.
 TITLE Targets for dioxin: genes for plasminogen activator inhibitor-2 and
 interleukin-1 beta
 JOURNAL Science 254 (5030), 415-418 (1991)
 REFERENCE 3 (bases 1 to 1723)
 MEDLINE Bradham, D.M., Igarashi, A., Potter, R.L. and Grotendorst, G.R.
 AUTHORS Connective tissue growth factor: a cysteine-rich mitogen secreted
 TITLE by human vascular endothelial cells is related to the SRC-induced
 immediate early gene product CEF-10
 JOURNAL J. Cell Biol. 114 (6), 1285-1294 (1991)
 REFERENCE 4 (bases 1 to 1900)
 MEDLINE 91373462
 JOURNAL

QY 361 accctgcggtgagttcaagtccctgacgagcgaggtcatgaaagaacatgatgttc 420
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DEFINITION Sequence 1 from patent US 5783187.
ACCESSION AR018957
VERSION AR018957.1 GI:3974071
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2075)
AUTHORS Grotendorst,G.R. and Bradham,D.M. Jr.
TITLE Treatment of cell proliferative disorders using antibodies which
bind connective tissue growth factor
JOURNAL Patent: US 5783187-A 1 21-JUL-1998;
FEATURES Location/Qualifiers
source
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ORIGIN
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DEFINITION Sequence 1 from Patent US 5408040.
ACCESSION I11636
VERSION I11636.1 GI:909154
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2075)
AUTHORS Grotendorst,G.R. and Bradham,D.M. Jr.
TITLE Connective tissue growth factor(CTGF).
JOURNAL Patent: US 5408040-A 1 18-APR-1995;
FEATURES Location/Qualifiers
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DEFINITION Sequence 1 from patent US 5585270.
ACCESSION I32210

Tue Aug 21 08:16:51 2001

J. Cell Biol. 114 (6), 1285-1294 (1995)
JOURNAL
MEDLINE
91373462
2 (bases 1 to 2075)
Grotendorst, G.R.
Direct Submission
Submitted (91-JUL-1990) Gary R. Grotendorst, Department of Cell
Biology and Anatomy, University Of Miami School of Medicine, Miami,
FL 33136, USA

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Db 1087 ATCAAGACCTGTCCTGCCATTACAACTGTCCCGGAGACATTGCTG
 Ov 481 tactacaggaagatgtacggagacatggca 510

1

21 Aug 21 08:16:51 2001

T32210.1 GI:1823001
VERSION
SYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
Unknown; 64,64

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

1 (bases 1 to 2075)
Grotendorst, G.R. and Bradham, D.M. Jr.
polynucleotides encoding connective tissue growth factor
Patent: US 5585270-A 1 17-DEC-1996;
Location/Qualifiers
1..2075

BASE COUNT	491 a	558 c	546 g	480 t
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[illegible]

QY 421 atcaagacctgtcctgcattacaccgctccggggttcccccttccttttgaatcgctg 1146
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Qy 481 tactacaggaagacacggag
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RESULT	5	PRI	05-MAR-1996
HUMCONGRO	2075 bp	mrna	
LOCUS		connective tissue growth factor,	complete cds.

DEFINITION M92934 M36965 S56201
ACCESSION M92934.1 GI:180923
VERSION growth factor; mitogen.
KEYWORDS Homo sapiens (library: lambda gtl) connective cDNA to mRNA.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.
1 (bases 1 to 2075)
REFERENCE Yaguchi, A., Potter, R.L. and Grotendorst, G.R. 1991. The human alpha-1-microglobulin gene: a polymorphic gene with a high degree of sequence conservation. *Gene* 104: 1-10.

AUTHORS BIAUMONT, J. and
TITLE Connective tissue growth factor: a Cys⁶⁸-rich protein whose expression is related to the SRC-induced tumorigenesis by human vascular endothelial cells is related to the immediate early gene product CEF-10

Db	1147	TACTACAGGAAGATGTACGGAGACATGGCA	1176
RESULT	6		
LOCUS	HSCTGF	2312 bp	10-MAR-1997
DEFINITION	H.sapiens mRNA for connective tissue growth factor.		
ACCESSION	X78947		
VERSION	X78947.1	GI:474933	
KEYWORDS	connective tissue; growth factor.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Oemar, B.S., Werner, A., Garnier, J.M., Do, D.D., Godoy, N., Nauck, M., Marz, W., Rupp, J., Pech, M. and Lüscher, T.F.		
TITLE	Human connective tissue growth factor is expressed in advanced atherosclerotic lesions		
JOURNAL	Circulation 95 (4), 831-839 (1997)		
MEDLINE	9720746		
REFERENCE	2 (bases 1 to 2312)		
AUTHORS	Oemar, B.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-APR-1994) B.S. Oemar, University Hospital Basel, Dept of Research, Lab of Vascular Research, Hebelstr. 20, 4031 Basel, SWITZERLAND		
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Qy	61	ctggtccagaccacagtgagcgcttttccaagacctgtgggatgggcatctccacc	120
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QY 61 ctggtccagaccacagagtgaggcgcttctccagacctgtgggatgggcatctccacc 120
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QY 1103 ACCCTTCCCGTGGAGTTCAGTGTCTCTGATGGGAGGTTCATGAAGAGAGCATGATGTT 1162
QY 421 atcaagacctgtcctgacattacaactgtcccgagacacatgacatcttgaatcgctg 480
QY 1163 ATCAAGACCTGTGCTGCCATTACACTGCGCGGAGAGCAATGACATCTTCGAGTCACTG 1222

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Matches 473; Conservative 0; Mismatches 36;
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LOCUS Bos taurus connective tissue growth factor precursor (CTGF) mRNA,
DEFINITION complete cds.
ACCESSION AF000137
VERSION AF000137.1 GI:2326193
KEYWORDS
SOURCE
ORGANISM cow, taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 2330)
Liljensiek, B., Lin, Z., Fotsis, T., Schimanski, M., Bierhaus, A.,
Kantiz, M., Kauffmann, G., Schweigerer, L., Ziegler, R. and
Nawroth, P.P.
Bos taurus connective tissue growth factor
Unpublished
2 (bases 1 to 2330)
Liljensiek, B., Lin, Z., Fotsis, T., Schimanski, M., Bierhaus, A.,
Kantiz, M., Kauffmann, G., Schweigerer, L., Ziegler, R. and
Nawroth, P.P.
Direct Submission
Submitted (17-APR-1997) Internal Medicine I, University of
Heidelberg, Im Neuenheimer Feld 324, 3. OG, R320 69120, Heidelberg
FEATURES
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SSU83916 1496 bp mRNA 12-AUG-1997
LOCUS Sus scrofa connective tissue growth factor (CTGF) mRNA, complete
DEFINITION cds.
ACCESSION U83916
VERSION U83916.1 GI:2317891
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1496)
AUTHORS Brigstock,D.R., Steffen,C.L., Kim,G.Y., Vegunta,R.K., Diehl,J.R.
and Harding,P.A.
TITLE Purification and characterization of novel heparin-binding growth
factors in uterine secretory fluids. Identification as
heparin-regulated Mr 10,000 forms of connective tissue growth
factor
JOURNAL J. Biol. Chem. 272 (32), 20275-20282 (1997)
MEDLINE 97390475
REFERENCE 2 (bases 1 to 1496)
AUTHORS Harding,P.A. and Brigstock,D.R.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1997) Surgery, Children's Hospital, 700
Children's Drive, Columbus, OH 43205, USA
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Tue Aug 21 08:16:51 2001

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RESULT 11
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LOCUS Mouse mRNA sequence.
DEFINITION
ACCESSION M80263
VERSION M80263.1 GI:201945
KEYWORDS transforming growth factor-beta.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2330)
AUTHORS Brunner, A., Chinn, J., Neubauer, M.G. and Purchio, A.F.
TITLE Identification of a gene family regulated by transforming growth factor-beta
JOURNAL DNA Cell Biol. 10, 293-300 (1991)
MEDLINE 91229699
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QY 481 tactacgagaatgtacgagacatggc 509
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DEFINITION complete cds.
ACCESSION AB023068
VERSION AB023068.1 GI:5360710
KEYWORDS connective tissue growth factor.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 2338)
AUTHORS Tezuka, K. and Tamatani, T.
TITLE Rattus norvegicus connective tissue growth factor
JOURNAL Published Only in Database (1999) In press
REFERENCE 2 (bases 1 to 2338)
AUTHORS Tezuka, K. and Tamatani, T.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-1999) to the DBJ/EMBL/GenBank databases.
Katsunari Tezuka, Pharmaceutical Frontier Research Laboratories, JT
Inc, Division of Molecular Immunology; 13-2, Fukuura

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1-chome,kanagawa-ku, Yokohama, Kanagawa 236-0004, Japan
(E-mail:katsunari.tesuka@ims.jti.co.jp, Tel:81-45-786-7693,
Fax:81-45-786-7692)

FEATURES
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Matches 462; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Db 924 AGCCCTGTGAAGCTGACCTAGAGAGAAACATTAAGAAGGGCAAAAAGTGCATCCCGAGC 983

QY 241 cccaaatctccaaacctatcaagtttgacgttcttggctgcaccagcatgaagacatac 300
Db 984 CCTAAATGCCAAGCCTGTCAAGTTTGAGCTTCTGGCTGCACCCAGTGTGAAGACCTAC 1043

QY 301 cgagctaaattctgtggagtatgacacgcgcgcgatgtgtgccccccacacagaccacc 360
Db 1044 CGGGCTAAGTTCTGTGGGTGTGTCACGGAGCGCGCTGCTGCACACCGCACAGACCACC 1103

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Db 1224 TACTACAGGAAGATGTATGAGACATGGC 1252

RESULT 13
AF120275
LOCUS
DEFINITION
Rattus norvegicus connective tissue growth factor mRNA, complete cds.
ACCESSION
AF120275
VERSION
AF120275.1 GI:5070343

KEYWORDS
SOURCE
ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 2345)
XU, J., Smock, S.L., Safadi, F.F., Rosenzweig, A.B., Odgren, P.R.,
Marks, S.C. Jr., Owen, T.A. and Popoff, S.N.
Cloning the full-length cDNA for rat connective tissue growth
factor: implications for skeletal development
J. Cell. Biochem. 77 (1), 103-115 (2000)
20145935
MEDLINE
PUBMED
10679821
REFERENCE
2 (bases 1 to 2345)
Smock, S.L. and Owen, T.A.
Direct Submission
Submitted (14-JAN-1999) Cardiovascular and Metabolic Diseases,
Prizer Central Research, Eastern Point Road, Groton, CT 06340, USA
3 (bases 1 to 2345)
XU, J., Rosenzweig, A.B., Safadi, F.F. and Popoff, S.N.
Direct Submission
Submitted (09-JUN-1999) Department of Anatomy and Cell Biology,
Temple University School of Medicine, 3400 North Broad Street,
Philadelphia, PA 19140, USA
4 (bases 1 to 2345)
Odgren, P.R. and Marks, S.C. Jr.
Direct Submission
Submitted (09-JUN-1999) Department of Cell Biology, University of
Massachusetts Medical School, 55 Lake Avenue North, Worcester, MA
01655, USA
FEATURES
source
1. .2345
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
225. .1268
/notes="CTGF"
/codon_start=1
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/translation="MLASVAGPVSLVLLVLLTRPATGDCSAQCCOCAAEEAPRCAG
VSLVLDGCGCCRVCAKQELCTERDPCDHPKGLFDFGSPANRKGVCATKDGAPCV
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EWVCDPDKDRTVVGPAALAYRLEDTFGDPTMMRANCLVQTTWESACSTCGMGISTR
VTNDTFCRLKQSLRCLWVRPCEADLEENIKKGCIRTPKIAKPVKFLSCTSVKT
YRAKFCGCTDGRCTPHRTTLLPVEFKPDGEIMKMMFIKTCACHNCPGNDIF
ESLYRKMYGDMA"
BASE COUNT 582 a 606 c 616 g 541 t
ORIGIN

Query Match 85.1%; Score 433.8; DB 94; Length 2345;
Best Local Similarity 90.8%; Pred. No. 9e-110;
Matches 462; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 ggcgttaccagactgaagacacgcttggccagaccacactatgattagagcaactgc 60
Db 756 GCTGCTTACCAATGAGACACATTTGGCCCTTGACCCAACTATGATGCGAGCAACTGC 815

QY 61 ctgttcagaccacagatggagcgcctgttccaaacacctgtggatggatcctccacc 120
Db 816 CTGCTCAGACCACAGATGGAGCGGCTGTCTAAGACCTGTGGATGGCATCTCCACC 875

QY 121 cgggttaccacatgacacgcctcctcagctagagaagcagagcgcgcctgtgcatggtc 180
Db 876 CGGGTTACCAATGAGACACATTTGCTGAGGCTGGAGAGCAGAGTCTCTCGATGGTC 935

QY 181 agccttgagaaactgacctggaagagaacattagaaggcgcaaaagtgcattccgtact 240
Db 936 AGCCCTGTGAAGCTGACCTAGAGAGAAACATTAAGAAGGGCAAAAAGTGCATCCCGAGC 995

QY 241 cccaaatctccaaacctatcaagtttgagcttctggtgcaccagcatgaagacatac 300

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YBAKFCGCTDRCCTPHRTATLPVEFCRCPDGEVMMKKMFIKTCACHYNCPGDNDIF
ESMYRKMIGDMA"
BASE COUNT 383 a 428 c 454 g 320 t
ORIGIN

Query Match		74.7%	Score 381;	DB 8;	Length 1585;
Best Local Similarity		84.3%	Pred. No. 4e-95;		
Matches 429;		Conservative 0;	Mismatches 80;	Indels 0;	Gaps 0;
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Db	568	GCTGTGTACAGACAGAGAGAAACCTATGGCCGGATCTTCCTTGATGGTGGCAACTGC	727		
QY	61	ctggctccagaccacagagtgagcgctgttccaaagacacctgtgggagtgagcattccacc	120		
Db	728	CTGGTCCAGACTACGGAAATGGAGTGGCTGCTCGAAGACATGGCGCATGGGCATCTCCACC	787		
QY	121	cggtttaccaatgacaacgcctcctcagggctagagaagcagagccgcctgtgcatggtc	180		
Db	788	AGGGTGACCAACGACAAATGAAATGTCTGACTGGAGAAACAGAGCCGCCCTGTGCATGGTC	847		
QY	181	aggccttgcaagctgacctggaagagacattaaagaagggaacaaagtgcattccgtact	240		
Db	848	AGACCTGTGAGGACGACACCTGGAGGAGACATTAAGAAAGGCAAGAGTGCAATCGTACC	907		
QY	241	cccaaatctccaagcctatcaagtttgagcttcttgctgaccagcagcatgaagacatac	300		
Db	908	CCCAAGATCTCCAAGCCAGTCAAGTTTGAAGTCTCTGGCTGCACACCGGTGAAGACATAC	967		
QY	301	cgagctaaattctgtgagtagtatgaccgagccgctgctgacccccccacagaaaccacc	360		
Db	968	CGCGCCCAAGTCTGCGGGGCTGTCACCGAGCGGCGTGTGTCACACCCACACAGAACCGCC	1027		
QY	361	accctgcgggtgagttcaagtgcctcagcgaggtcatgaagaacatgatgttc	420		
Db	1028	ACCTGCCCCGTGGAGTTCAGTCCCGCGAGCGGCGGTGATGAAGAGAAAGATGATGTTTC	1087		
QY	421	atcaagacctgtgcctgacattacaactgtcccggagacaatgacatctttgaatcgctg	480		
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QY	481	tactacaggaagatgtacggagacatggc	509		
Db	1148	TACTACAGGAAGATGTACGGGGACATGGC	1176		

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Job time: 2352 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2001, 21:25:44 ; Search time 127.58 Seconds
(without alignments)
2510.032 Million cell updates/sec

Title: US-09-461-646-1_COPY_667_1176

Perfect score: 510

Sequence: 1 gcgcctaccgactggaaga.....agatgtacggagacatggca 510

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510	100.0	1415	21	AA11281 Human connective t
2	510	100.0	2075	16	AAT04226 Connective tissue
3	510	100.0	2075	18	AAT45360 Human connective t
4	510	100.0	2075	18	AAT51234 Connective tissue
5	510	100.0	2075	19	AAT38085 Human connective t
6	510	100.0	2075	20	AA61317 Human connective t
7	510	100.0	2075	21	AA11278 Human connective t
8	510	100.0	2075	21	AA11280 Human connective t
9	510	100.0	2075	22	AAT59954 Human connective t
10	510	100.0	2075	22	AAC87517 Human connective t
11	433.8	85.1	2267	18	AAT94700 Murine Fisp12 cDNA

12	433.8	85.1	2330	13	AAQ26422	Gene for beta-IG-M
13	433.8	85.1	2338	20	AAAX90030	Rat connective tis
14	427.4	83.8	2350	21	AA115477	Clone 2-4-7 encodi
15	299.4	58.7	2553	21	AAV78039	Human cancer assoc
16	296.4	58.1	4212	20	AAV65380	Connective tissue
17	296.4	58.1	4214	18	AAT59618	Connective tissue
18	296.4	58.1	4214	18	AAT58534	Human connective t
19	287.2	56.3	486	22	AAF2294	Bovine mammary tis
20	286.4	56.2	488	20	AAAX29126	Polynucleotide RFP
21	283.4	55.6	341	21	AA50437	Mouse connective t
22	280.2	54.9	341	21	AA50436	Rat connective tis
23	180	35.3	1975	14	AAQ36031	Chicken nov coding
24	157.2	30.8	1146	18	AAT97142	Human monocyte mat
25	157.2	30.8	1418	18	AAT94699	Human cysteine ric
26	157.2	30.8	2270	21	AAAX98875	Human proliferatio
27	157.2	30.8	2270	21	AAAX98157	Human proliferatio
28	157.2	30.8	2307	21	AAAX78196	Human cancer assoc
29	155.6	30.5	1128	17	AAT12553	Connective tissue
30	153	30.0	1128	20	AAZ11720	Human CTGF-2 cDNA
31	150.8	29.6	2028	13	AAQ26421	Gene for beta-IG-M
32	144.8	28.4	1062	20	AAZ11246	Human connective t
33	135	26.5	1101	20	AAAX76483	Human WISP-1 prote
34	135	26.5	1140	20	AAAX76485	Mouse WISP-1 prote
35	135	26.5	1183	20	AAAX76494	Human WISP-1 clone
36	135	26.5	1403	20	AAAX76490	Human WISP-1 clone
37	135	26.5	1766	20	AAAX76484	Mouse WISP-1 prote
38	135	26.5	2795	22	AAAC91577	Human PRO342 cDNA
39	135	26.5	3658	21	AAZ58613	Human connective t
40	133.4	26.2	2830	20	AAAX76482	Human WISP-1 prote
41	129.4	25.4	619	14	AAQ36046	Human sequence XXV
42	122	23.9	546	20	AAAX76495	Human WISP-1 clone
43	122	23.9	683	20	AAAX76492	Human WISP-1 clone
44	119.2	23.4	1142	20	AAZ11245	Human connective t
45	119.2	23.4	1183	21	AAA06928	Human growth facto

ALIGNMENTS

RESULT 1
AA11281
ID AA11281 standard; cDNA; 1415 BP.
XX
AC AA11281;
XX
DT 08-NOV-2000 (first entry)
XX
DE Human connective tissue growth factor partial cDNA.
XX
KW Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;
KW fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;
KW hypertrophic scarring; atherosclerosis; diabetic nephropathy; retinopathy;
KW hypertension; cardiovascular disorder; wound healing; bone repair; ss.
XX
OS Homo sapiens.
XX
PN WO200035939-A2.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-US29654.
XX
PR 14-DEC-1998; 98US-0112240.
XX
PR 14-DEC-1998; 98US-0112241.
XX
PA (UYMI-) UNIV MIAMI.
XX
PA (FIBR-) FIBROGEN INC.
XX
PI Grotendorst GR, Neff TB;
XX
DR WPI; 2000-431568/37.
XX
DR P-PSDB; AAY92941.

Db 967 cgagctaaattctgtgagtatgtacgagcgccgagtgctgcacccccacagaaccacc 1026
 QY 361 accctgcggtgaggttcaagtccctgacgagcgaggtcatgaagaacaatgatgttc 420
 Db 1027 accctgcggtgaggttcaagtccctgacgagcgaggtcatgaagaacaatgatgttc 1086
 QY 421 atcaagacctgtgcctgacctcaactgacctcccgagagacaatgacatctttgtaatgcgtg 480
 Db 1087 atcaagacctgtgcctgacctcaactgacctcccgagagacaatgacatctttgtaatgcgtg 1146
 QY 481 tactacaggaagatgtacggagacatggca 510
 Db 1147 tactacaggaagatgtacggagacatggca 1176

RESULT 3
 AAT45360
 ID AAT45360 standard; cDNA; 2075 BP.
 XX
 AC AAT45360;
 XX
 DT 26-APR-1997 (first entry)
 XX
 DE Human connective tissue growth factor cDNA.
 XX
 KW Connective tissue growth factor; CTGF; mitogen; cell proliferation;
 KW wound healing; cancer; tumor; fibrosis; glaucoma; atherosclerosis;
 KW diagnosis; therapy; antisense; triple helix; ribozyme; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 130..1179
 FT /*tag= a
 XX
 PN WO9638172-A1.
 XX
 XX 05-DEC-1996.
 XX
 XX 31-MAY-1996; 96WO-0508140.
 XX
 PR 31-MAY-1996; 96WO-0508140.
 XX
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Bradham DM, Grotendorst GR;
 XX
 XX WPI; 1997-042659/04.
 DR P-PSDB; AAW09089.
 XX
 XX Connective tissue growth factor coding sequence and protein - used
 PT in the treatment of proliferative disorders and to accelerate wound
 PT healing
 XX
 PS Claim 20; Page 50-52; 76pp; English.
 XX
 CC A cDNA clone (AAT45360) codes for novel human connective tissue growth
 CC factor (CTGF) (AAW09089), a PDGF-immunorelated protein that may play a
 CC significant role in the normal development, growth and repair of
 CC human tissue and which probably functions as a growth factor in
 CC wound healing. CTGF may be involved in diseases in which there is
 CC an overgrowth of connective tissue cells, such as cancer, tumour
 CC formation and growth, fibrotic diseases (e.g. pulmonary fibrosis,
 CC kidney fibrosis, glaucoma) and atherosclerosis. The cDNA clone was
 CC isolated from a HUVEC cDNA library using anti-PDGF antibody. CTGF
 CC nucleic acids can be used for recombinant prodn. of CTGF and as
 CC probes to detect CTGF mRNA. CTGF genomic DNA (AAT58534) has also
 CC been isolated. A proliferative disorder may be treated using e.g.
 CC a CTGF antisense, ribozyme or triplex agent.
 XX
 SI Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;

Query Match 100.0%; Score 510; DB 18; Length 2075;
 Best Local Similarity 100.0%; Pred. No. 1..1e-144;
 Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttacgactggaagacacagctgttggcccgagaccacactatgattagagcaactgc 60
 Db 667 gcggcttacgactggaagacacagctgttggcccgagaccacactatgattagagcaactgc 726
 QY 61 ctggtccagaccacagagtgagcgctgttccaagacctgtggagtggtgcatctccacc 120
 Db 727 ctggtccagaccacagagtgagcgctgttccaagacctgtggagtggtgcatctccacc 786
 QY 121 cgggttaccaatgacaacgcctctcctcaggtctagagagcagagcccgctgtgcatggtc 180
 Db 787 cgggttaccaatgacaacgcctctcctcaggtctagagagcagagcccgctgtgcatggtc 846
 QY 181 aggccttgcaagctgacctggaagagaacattaaaggggcaaaaagtgcactcgtact 240
 Db 847 aggccttgcaagctgacctggaagagaacattaaaggggcaaaaagtgcactcgtact 906
 QY 241 cccaaaatctccaaagcctatcaagtttgaagtttctgctgcaccagcatgaagacatac 300
 Db 907 cccaaaatctccaaagcctatcaagtttgaagtttctgctgcaccagcatgaagacatac 966
 QY 301 cgagctaaattctgtgagtgatgtaccgacggccgagtgctgcacccccacagaaccacc 360
 Db 967 cgagctaaattctgtgagtgatgtaccgacggccgagtgctgcacccccacagaaccacc 1026
 QY 361 accctgcggtgaggttcaagtgacctgacggcgaggtctcatgaagaagaacatgatgttc 420
 Db 1027 accctgcggtgaggttcaagtgacctgacggcgaggtctcatgaagaagaacatgatgttc 1086
 QY 421 atcaagacctgtgcctgccattacaactgtcccggagacaatgacatctttgtaatgcgtg 480
 Db 1087 atcaagacctgtgcctgccattacaactgtcccggagacaatgacatctttgtaatgcgtg 1146
 QY 481 tactacaggaagatgtacggagacatggca 510
 Db 1147 tactacaggaagatgtacggagacatggca 1176

RESULT 4
 AAT51234
 ID AAT51234 standard; cDNA; 2075 BP.
 XX
 AC AAT51234;
 XX
 DT 18-MAR-1997 (first entry)
 XX
 DE Connective tissue growth factor coding sequence.
 XX
 KW Connective tissue growth factor; CTGF; human; connective tissue cell;
 KW proliferative disease; platelet-derived growth factor; PDGF; development;
 KW tissue growth; repair; umbilical vein endothelial cell; HUVE cell;
 KW antibody; wound healing; cancer; fibrotic disease; atherosclerosis;
 KW inhibitor; protease degradation; growth factor; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 130..1179
 FT /*tag= a
 FT /product= connective tissue growth factor
 XX
 PN US5585270-A.
 XX
 PD 17-DEC-1996.
 XX
 PF 30-AUG-1991; 91US-0752427.
 XX
 PR 30-AUG-1991; 91US-0752427.
 PR 14-DEC-1993; 93US-0167628.
 PR 10-FEB-1995; 95US-0386680.

Db 787 cgggttaccgaatgacacgcccctctcagctagagaagcagagccgctgtgcatggtc 846
 Qy 181 aggccttgcgaagctgacctggaagagaacattaaagaaggcgaagaaagtgatcccgtaact 240
 Db 847 aggccttgcgaagctgacctggaagagaacattaaagaaggcgaagaaagtgatcccgtaact 906
 Qy 241 cccaaatctccaaagcctatcaagtttgagctttctggtgcaccgagcatgaagacatac 300
 Db 907 cccaaatctccaaagcctatcaagtttgagctttctggtgcaccgagcatgaagacatac 966
 Qy 301 cgaagctaaattctgtgagatgtaccgagcggccgagctgtgaccccccaagaaacacc 360
 Db 967 cgaagctaaattctgtgagatgtaccgagcggccgagctgtgaccccccaagaaacacc 1026
 Qy 361 accctgcgggtgagttcaagtgcctgcgagcggaggttcataagaagaacatgatgttc 420
 Db 1027 accctgcgggtgagttcaagtgcctgcgagcggaggttcataagaagaacatgatgttc 1086
 Qy 421 atcaagacctgtgcctgccattacaactgtcccgagagacaatgacatctttgaaatcgctg 480
 Db 1087 atcaagacctgtgcctgccattacaactgtcccgagagacaatgacatctttgaaatcgctg 1146
 Qy 481 tactacaggaagatgtacggagacatggca 510
 Db 1147 tactacaggaagatgtacggagacatggca 1176

RESULT 6

AA11278
 ID AAX61317 standard; cDNA; 2075 BP.

AC AAX61317;

DT 20-AUG-1999 (first entry)

DE Human connective tissue growth factor coding sequence.

KW CTGF; connective tissue growth factor; human; fibrotic disease;

KW cell proliferative disorder; atherosclerosis; diagnosis; ss.

OS Homo sapiens.

XX US5916756-A.

PN 29-JUN-1999.

XX 20-JUN-1997; 97US-0880031.

PF 14-DEC-1993; 93US-0167628.

PR 10-FEB-1995; 95US-0386680.

PR 11-SEP-1996; 96US-0712302.

PR 20-JUN-1997; 97US-0880031.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Bradham DM, Grotendorst GR;

XX WPI: 1999-384720/32.

DR P-PSDB; AAY18361.

XX Detecting cell proliferative disorders such as fibrotic disease and

XX atherosclerosis

XX Disclosure; Column 15-18; 11pp; English.

XX This sequence encodes the human connective tissue growth factor (CTGF).

XX The invention relates to a method of detecting a cell proliferative

XX disorder comprising comparing the level of CTGF in a sample against a

XX control, where an increase is indicative of a cell proliferative disorder

XX (fibrotic disease or atherosclerosis). The method is used to detect cell

SQ Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;

Query Match 100.0%; Score 510; DB 20; Length 2075;

Best Local Similarity 100.0%; Pred No. 1,1e-144;

Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcggttaccgactggaagacacgctttggccagaccacactatgattagagcaactgc 60
 Db 667 gcggttaccgactggaagacacgctttggccagaccacactatgattagagcaactgc 726
 Qy 61 ctggtccagaccacagagtgagcgcctgttccaaagacctgtgggagcatctccacc 120
 Db 727 ctggtccagaccacagagtgagcgcctgttccaaagacctgtgggagcatctccacc 786
 Qy 121 cgggtttaccaaatgacaacgcctctcagctagagaagcagagccgctgtgcatggtc 180
 Db 787 cgggtttaccaaatgacaacgcctctcagctagagaagcagagccgctgtgcatggtc 846
 Qy 181 agccttgcgaagctgacctggaagagaacattaaagaaggcgaagaaagtgatcccgtaact 240
 Db 847 agccttgcgaagctgacctggaagagaacattaaagaaggcgaagaaagtgatcccgtaact 906
 Qy 241 cccaaatctccaaagcctatcaagtttgagctttctggtgcaccgagcatgaagacatac 300
 Db 907 cccaaatctccaaagcctatcaagtttgagctttctggtgcaccgagcatgaagacatac 966
 Qy 301 cgaagctaaattctgtgagatgtaccgagcggccgagctgtgaccccccaagaaacacc 360
 Db 967 cgaagctaaattctgtgagatgtaccgagcggccgagctgtgaccccccaagaaacacc 1026
 Qy 361 accctgcgggtgagttcaagtgcctgcgagcggaggttcataagaagaacatgatgttc 420
 Db 1027 accctgcgggtgagttcaagtgcctgcgagcggaggttcataagaagaacatgatgttc 1086
 Qy 421 atcaagacctgtgcctgccattacaactgtcccgagagacaatgacatctttgaaatcgctg 480
 Db 1087 atcaagacctgtgcctgccattacaactgtcccgagagacaatgacatctttgaaatcgctg 1146
 Qy 481 tactacaggaagatgtacggagacatggca 510
 Db 1147 tactacaggaagatgtacggagacatggca 1176

RESULT 7

AA11278
 ID AAA11278 standard; cDNA; 2075 BP.

AC AAA11278;

DT 08-NOV-2000 (first entry)

DE Human connective tissue growth factor cDNA.

XX

Dermatological; antiarthritic; antiarteriosclerotic; antidiabetic;
 nephrotropic; ophthalmological; hypotensive; cardiac; tranquilizer;
 vulnary; antiinflammatory; human; connective tissue growth factor;
 CTGF; extracellular matrix synthesis; collagen synthesis; antibody;
 myofibroblast differentiation; antisense; fibroproliferative disease;
 fibrosis; trauma; cancer; inflammation; diabetes; keloid; ss.

OS Homo sapiens.

XX WO200035936-A1.

PN 22-JUN-2000.

XX 14-DEC-1999; 99WO-US29652.

XX 14-DEC-1998; 98US-0112240.

PR 14-DEC-1998; 98US-0112241.

XX (UYMI-) UNIV MIAMI.

us-09-461-646-1_copy_667_1176.rng

Tue Aug 21 08:16:51 2001

XX
PI Grotendorst GR;
XX WPI; 2000-431565/37.
XX P-PSDB; AAY92939.
XX
XX Fragment of connective tissue growth factor, useful for treating
XX fibroproliferative diseases or disorders, including kidney fibrosis, diabetic
XX scleroderma, arthritis, hypertrophic scarring, atherosclerosis, diabetic
XX nephropathy and retinopathy
XX
XX Disclosure; Fig 3A-B; 74pp; English.
XX
XX This sequence represents the full coding sequence for the human
XX connective tissue growth factor (CTGF) polypeptide having the ability
XX to induce extracellular matrix synthesis, collagen synthesis and/or
XX myofibroblast differentiation. The invention relates to fragments of
XX CTGF, especially those encoded by exons 2 and/or 3, which contain the
XX inductive activity. The protein and/or fragments can be used to raise
XX antibodies and the coding sequence can be used to generate antisense
XX oligonucleotides. The antibody or antisense sequence against the CTGF
XX sequence can be used in a method to treat a CTGF-associated disease or
XX disorder such as a fibroproliferative disease or disorder, especially
XX selected from kidney fibrosis, scleroderma, pulmonary fibrosis, diabetic
XX fibrosis, arthritis, hypertrophic scarring, atherosclerosis, diabetic
XX nephropathy and retinopathy, hypertension, kidney disorders, and
XX angiogenesis-related disorders. The disease or disorder can also be selected
XX from cardiovascular diseases (including surgery or radiation therapy,
XX from acute or repetitive traumas (including cancers), inflammatory bowel
XX disease, Crohn's disease, joint inflammation, interstitial disease,
XX dermatological diseases, diabetes, and keloids.
XX
XX Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 510; DB 21; Length 2075;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-144;
XX Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ggggttaccgactggaagacacgtttggccagacacactatgattagagccactgc 60
XX Db 667 ggggttaccgactggaagacacgtttggccagacacactatgattagagccactgc 726
XX
XX QY 61 ctggttcagacacagactgagcgccctgttccaaagacctgtggatgggcatctccacc 120
XX Db 727 ctggttcagacacagactgagcgccctgttccaaagacctgtggatgggcatctccacc 786
XX
XX QY 121 cgggttaccaatgacaacgctctctgagcgctgttccaaagacctgtggatgggcatctccacc 180
XX Db 787 cgggttaccaatgacaacgctctctgagcgctgttccaaagacctgtggatgggcatctccacc 846
XX
XX QY 181 aggccttcgaagctgacctggaagagacattgaagagggcacaagagtcactcgact 240
XX Db 847 aggccttcgaagctgacctggaagagacattgaagagggcacaagagtcactcgact 906
XX
XX QY 241 cccaaatctccagcctatcaagtttgactttctgctgaccagcatgaagacatac 300
XX Db 907 cccaaatctccagcctatcaagtttgactttctgctgaccagcatgaagacatac 966
XX
XX QY 301 cagagtaattctgtgagtagtgatgacgagcgccgctgacccccacagacaccacc 360
XX Db 967 cagagtaattctgtgagtagtgatgacgagcgccgctgacccccacagacaccacc 1026
XX
XX QY 361 acccttcgctggagttcaagtcacctgacgagcgaggttcattgaagaagacatgatgttc 420
XX Db 1027 acccttcgctggagttcaagtcacctgacgagcgaggttcattgaagaagacatgatgttc 1086
XX
XX QY 421 atcaagacctgtgctgacattacaactgtcccgagacacatgacattctttgaatcgctg 480
XX Db 1087 atcaagacctgtgctgacattacaactgtcccgagacacatgacattctttgaatcgctg 1146

QY 481 tactacaggaagatgtacggagacatggca 510
Db 1147 tactacaggaagatgtacggagacatggca 1176
RESULT 8
AA11280 ID AA11280 standard; cDNA; 2075 BP.
XX AA11280;
XX 08-NOV-2000 (first entry)
XX Human connective tissue growth factor cDNA.
XX Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;
XX fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;
XX hypertrophic scarring; atherosclerosis; diabetic nephropathy; retinopathy;
XX hypertension; cardiovascular disorder; wound healing; bone repair; ss.
XX Homo sapiens.
XX Location/Qualifiers
XX Key 130..1179
XX CDS /tag= a
XX /product= "connective tissue growth factor"
XX WO200035939-A2.
XX 22-JUN-2000.
XX 14-DEC-1999; 99WO-US29654.
XX 14-DEC-1998; 98US-0112240.
XX 14-DEC-1998; 98US-0112241.
XX (UYMI-) UNIV MIAMI.
XX (FIBR-) FIBROGEN INC.
XX Grotendorst GR, Neff TB;
XX WPI; 2000-431568/37.
XX P-PSDB; AAY92940.
XX New fragment of connective tissue growth factor (CTGF) polypeptide
XX having mitogenic activity, useful in wound healing, bone and tissue
XX repair
XX Disclosure; Fig 2A-B; 71pp; English.
XX This sequence represents the full length coding sequence for the human
XX connective tissue growth factor (CTGF) polypeptide which has mitogenic
XX activity. The protein can be used to raise antibodies which specifically
XX bind to CTGF and are used to treat a CTGF-associated disease or disorder,
XX e.g. a fibroproliferative disease/disorder such as kidney fibrosis,
XX scleroderma, pulmonary fibrosis, liver fibrosis, arthritis, hypertrophic
XX scarring, atherosclerosis, diabetic nephropathy and retinopathy, skin
XX hypertension, kidney disorders, angiogenesis-related disorders, skin
XX fibrotic disorders, and cardiovascular disorders. The protein is also
XX useful in wound healing, bone and tissue repair.
XX Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;
XX SQ
Query Match 100.0%; Score 510; DB 21; Length 2075;
Best Local Similarity 100.0%; Pred. No. 1.1e-144;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ggggttaccgactggaagacacgtttggccagacacactatgattagagccactgc 60
Db 667 ggggttaccgactggaagacacgtttggccagacacactatgattagagccactgc 726
QY 61 ctggttcagacacagactgagcgccctgttccaaagacctgtggatgggcatctccacc 120
Db 727 ctggttcagacacagactgagcgccctgttccaaagacctgtggatgggcatctccacc 786
QY 121 cgggttaccaatgacaacgctctctgagcgctgttccaaagacctgtggatgggcatctccacc 180
Db 787 cgggttaccaatgacaacgctctctgagcgctgttccaaagacctgtggatgggcatctccacc 846
QY 181 aggccttcgaagctgacctggaagagacattgaagagggcacaagagtcactcgact 240
Db 847 aggccttcgaagctgacctggaagagacattgaagagggcacaagagtcactcgact 906
QY 241 cccaaatctccagcctatcaagtttgactttctgctgaccagcatgaagacatac 300
Db 907 cccaaatctccagcctatcaagtttgactttctgctgaccagcatgaagacatac 966
QY 301 cagagtaattctgtgagtagtgatgacgagcgccgctgacccccacagacaccacc 360
Db 967 cagagtaattctgtgagtagtgatgacgagcgccgctgacccccacagacaccacc 1026
QY 361 acccttcgctggagttcaagtcacctgacgagcgaggttcattgaagaagacatgatgttc 420
Db 1027 acccttcgctggagttcaagtcacctgacgagcgaggttcattgaagaagacatgatgttc 1086
QY 421 atcaagacctgtgctgacattacaactgtcccgagacacatgacattctttgaatcgctg 480
Db 1087 atcaagacctgtgctgacattacaactgtcccgagacacatgacattctttgaatcgctg 1146

Db 727 ctggtccagaccacagagtgagcgctgtccagacacctgtggatgggcatctccacc 786
QY 121 cgggttaccacagacacccctctcagcctagagaaagcagacgacctgtgcatggtc 180
Db 787 cgggttaccacagacacccctctcagcctagagaaagcagacgacctgtgcatggtc 846
QY 181 aggccttgcgaagctgacctggaagagacattaaagagggcaaaaagtgcacctact 240
Db 847 aggccttgcgaagctgacctggaagagacattaaagagggcaaaaagtgcacctact 906
QY 241 cccaaatctccaaagcctatcaagtttgagcttcttggtgacccagcatgaagacatac 300
Db 907 cccaaatctccaaagcctatcaagtttgagcttcttggtgacccagcatgaagacatac 966
QY 301 cgaagctaaattctgtgagatgtatgacagcggccgagctgctgacccccacagacacc 360
Db 967 cgaagctaaattctgtgagatgtatgacagcggccgagctgctgacccccacagacacc 1026
QY 361 accctgcccgtgagttcaagtgcctgacgagcggaggttcagagacacatgatttc 420
Db 1027 accctgcccgtgagttcaagtgcctgacgagcggaggttcagagacacatgatttc 1086
QY 421 atcaagacctgtgctgctccattacaactgtcccgagagacacatgatttcgattc 480
Db 1087 atcaagacctgtgctgctccattacaactgtcccgagagacacatgatttcgattc 1146
QY 481 tactacaggaagatgtacggagacatggca 510
Db 1147 tactacaggaagatgtacggagacatggca 1176

RESULT 9

AAF59954
ID AAF59954 standard; cDNA; 2075 BP.

XX AC AAF59954;
XX DT 22-MAY-2001 (first entry)

XX DE Human connective tissue growth factor (CTGF) cDNA.
XX DE Human CTGF; connective tissue growth factor; recombinant production;
XX DE mitogenic; chemotactic; tissue development; growth; repair;
XX DE wound healing; vulnary; diagnostic agent;
XX DE cellular proliferation disorder; ss.

XX OS Homo sapiens.

XX XX US6190884-B1.

XX PN 20-FEB-2001.

XX PD 18-MAY-1998; 98US-0080715.

XX PF 14-DEC-1993; 93US-0167628.

XX PR 10-FEB-1995; 95US-0386680.

XX PR 30-AUG-1991; 91US-0752427.

XX PR 11-SEP-1996; 96US-0712302.

XX XX (UYSF-) UNIV SOUTH FLORIDA.

XX XX Grotendorst GR, Bradham DM;

XX XX WPI: 2001-210379/21.

XX XX P-PSDB; AAB60664.

XX XX Producing connective tissue growth factor involves transforming a host

XX XX cell with polynucleotide encoding the growth factor and growing the

XX XX cell under optimum conditions so that the polynucleotide is expressed

XX XX

XX XX Claim 9; Column 15-18; 11pp; English.

XX CC The invention relates to a method for the recombinant production of
CC human connective tissue growth factor (CTGF; AAB60664), involving
CC transforming a prokaryotic or eukaryotic host cell with an expression
CC construct comprising the CTGF cDNA sequence (AAF59954) or a fragment
CC thereof, and culturing the host cell under conditions suitable for the
CC expression of CTGF. CTGF is a mitogen and chemotactic agent for
CC connective tissue cells and plays a significant role in normal
CC development, growth and repair of human tissues. It is useful as a
CC therapeutic for accelerating wound healing and promoting normal healing
CC mechanisms and may therefore be used in the treatment of e.g., burns.
CC CTGF is also useful as a diagnostic reagent for diagnosing pathological
CC states in a patient suspected of having a disease characterised by a
CC disorder of cellular proliferation. The present sequence represents
CC cDNA encoding human CTGF.
XX SQ Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;

Query Match 100.0%; Score 510; DB 22; Length 2075;
Best Local Similarity 100.0%; Pred NO. 1,1e-144;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggttaccgactggaagacacgtttggccagaccacacattgattagagccaaactgc 60
Db 667 gcggttaccgactggaagacacgtttggccagaccacacattgattagagccaaactgc 726
QY 61 ctggtccagacacacagagtgagcgctgttccaaagacctgtggatgggcatctccacc 120
Db 727 ctggtccagacacacagagtgagcgctgttccaaagacctgtggatgggcatctccacc 786
QY 121 cgggtttaccaatgacacgcctcctcagcctagagaaagcagacgacctgtgcatggtc 180
Db 787 cgggtttaccaatgacacgcctcctcagcctagagaaagcagacgacctgtgcatggtc 846
QY 181 aggccttgcgaagctgacctggaagagacattaaagagggcaaaaagtgcacctact 240
Db 847 aggccttgcgaagctgacctggaagagacattaaagagggcaaaaagtgcacctact 906
QY 241 cccaaatctccaaagcctatcaagtttgagcttcttggtgacccagcatgaagacatac 300
Db 907 cccaaatctccaaagcctatcaagtttgagcttcttggtgacccagcatgaagacatac 966
QY 301 cgaagctaaattctgtgagatgtatgacagcggcagctgctgacccccacagacacc 360
Db 967 cgaagctaaattctgtgagatgtatgacagcggcagctgctgacccccacagacacc 1026
QY 361 accctgcccgtgagttcaagtgcctgacgagcggaggttcagagacacatgatttc 420
Db 1027 accctgcccgtgagttcaagtgcctgacgagcggaggttcagagacacatgatttc 1086
QY 421 atcaagacctgtgctgctccattacaactgtcccgagagacacatgatttcgattc 480
Db 1087 atcaagacctgtgctgctccattacaactgtcccgagagacacatgatttcgattc 1146
QY 481 tactacaggaagatgtacggagacatggca 510
Db 1147 tactacaggaagatgtacggagacatggca 1176

RESULT 10

AAC87517

ID AAC87517 standard; cDNA; 2075 BP.

XX AC AAC87517;
XX DT 09-MAR-2001 (first entry)

XX DE Human connective tissue growth factor (CTGF) cDNA.
XX DE Human; connective tissue growth factor; CTGF; PDGF-like activity;
XX DE platelet-derived growth factor; transforming growth factor-beta;
XX DE TGF-beta; mitogenic; proliferative; chemotactic; wound healing;

RESULT 13
X90030
AAX90030 standard; DNA: 2338 BP.

AAX90030:
17-SEP-1999 (first entry)
Rat connective tissue growth factor encoding DNA.
Human; monoclonal antibody; connective tissue growth factor; CTGF;
cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
rheumatic vascular inflammation; ss.
Rattus sp.
WO9933878-A1.
08-JUL-1999.
16-DEC-1998; 98WO-JP05697.
15-DEC-1998; 98JP-0356183.
25-DEC-1997; 97JP-0367699.
(NIBS) JAPAN TOBACCO INC.
Sakamoto S, Takigawa M, Tamatani T, Tezuka K;
WPI: 1999-430232/36.
P-PSDB; AAY24379.
New monoclonal antibody reactive with connective tissue growth
factor useful in the treatment of cell proliferation disorders
Claim 62; Page 161-166; 213pp; Japanese.
AAX90020 to AAX90029 encode monoclonal antibodies which react with human
connective tissue growth factor (CTGF). AAY24369 to AAY24378 represent
these monoclonal antibodies. The antibodies are useful in the diagnosis,
prevention and treatment of cell proliferation disorders in which CTGF
is implicated, including fibrosis of lung, kidney, liver and other
tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid
arthritis; rheumatic vascular inflammation; hepatitis; and cancer.
The present sequence encodes rat CTGF.

Sequence 2338 BP; 579 A; 602 C; 617 G; 538 T; 2 other;

Query Match	85.1%	Score 433.8;	DB 20;	Length 2338;
Best Local Similarity	90.8%;	Pred. NO. 1.4e-121;		
Matches 462;	Conservative	0;	Mismatches 47;	Indels 0;
Gaps				
QY 1	gcggcttcacgactggaagacacgtttgcccagagaccactatgtagagccaactgc 60			
DB 744	gctgcctaccgactggaagacacattggccctaccacactatgatgcgagccaactgc 803			
QY 61	ctggtccagaccagagtggaagcgcctgttccaaagacctgtgggatggcatctccacc 120			
DB 804	ctggtccagaccagagtggaagcgcctgttccaaagacctgtgggatggcatctccacc 863			
QY 121	cgggtttaccaatgacaacgctctcagcctgagtagaagacagagccgctgtgcatacgttc 180			
DB 864	cgggtttaccaatgacaacgctctcagcctgagtagaagacagagctcgtctcgtatcgttc 923			
QY 181	agccttcggaagctgacctgggaagagacatttagaaggcaaaagtgcattccgtact 240			
DB 924	agccttcggaagctgacctgggaagagacatttagaaggcaaaagtgcattccgtact 983			
QY 241	cccaaaatccaaagcctatcaagtttgagcttttgcctgcaccagatgaagacatac 300			
DB 984	cctaaatgccaagcctgtcaagtttgagcttttgcctgcaccagtgtagaacatac 1043			

```
CC detect expression of CTGF in a sample.
XX
SQ Sequence 2350 BP; 583 A; 616 C; 610 G; 541 T; 0 other;

Query Match      83.8%; Score 427.4; DB 21; Length 2350;
Best Local Similarity 90.0%; Pred. No. 1.2e-119;
Matches 458; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 gcggctaccgactggaagacagctgttggccagaccacactatgattagaccactgc 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 743 gctgctaccgactggaagacacatttggccctgacccaactatgctgcagccactgc 802
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ctggtccagaccacagagtgagcgctgttccaagaccctgtggtggtggtccacc 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 803 ctggtccagaccacagagtgagcgctgttccaagaccctgtggtggtggtccacc 862
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 cgggttaccatgacacgcctctcctgagctagagagagagagagccctgtgcatggtc 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 863 cgggttaccatgacacgcctctcctgagctagagagagagagagagagagagagagag 922
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 aggccttgcgaagctgacctgggaagagacattaaagagggcaaaaagtgcactcgtact 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 923 aggccttgcgaagctgacctgggaagagacattaaagagggcaaaaagtgcactcgtact 982
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 cccaaaatctccaaagcctatcaagtttgagcttcttctgctgcaccagcatgaagacatac 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 983 cctaaaattgccaaagcctgctcaagtttgagcttcttctgctgcaccagcatgaagacatac 1042
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 cgaagctaaattctgagtagtatgacacgagcgccgtagtgcacccccccacagaccacc 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1043 cgggtaagtctgtggtgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1102
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 accctgcggtggaagctcaagtcagtcgagcgagagagagagagagagagagagagagagag 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1103 acactgcggtggaagctcaagtcagtcgagcgagagagagagagagagagagagagagagag 1162
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 atcaagaccctgtgctgctccattcaaaatgctcccgagagacatgacatcttttgaatcgtg 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1163 atcaagaccctgtgctgctccattcaaaatgctcccgagagacatgacatcttttccgtgatg 1222
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 tactacaggaagatgtacgagacatggc 509
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1223 tactacaggaagatgtacgagacatggc 1251
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
AAC78039
ID AAC78039 standard; cDNA; 2553 BP.
AC
AC AAC78039;
XX
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated gene sequence SEQ ID NO:433.
XX
XX Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotrophic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; hematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW hemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200055350-A1.
XX
XX 21-SEP-2000.
XX
```

08-MAR-2000; 2000WO-US05882.
12-MAR-1999; 99US-0124270.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM;
P-PSDB; AAB43830.
WPI; 2000-587533/55.
Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
Claim 1; Page 974-975; 2352pp; English.
AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnery; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
nootropic; vasotrophic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of the present invention.
Sequence 2553 BP; 700 A; 569 C; 584 G; 689 T; 11 other;
Query Match 58.7%; Score 299.4; DB 21; Length 2553;
Best Local Similarity 99.7%; Pred. No. 7.5e-81;
Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 210 cattaaagaaggcgaagagtgatccctactctcccaaaatctccaaagcctatcaagtttga 269
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1070 ccttaagaaggcgaagagtgatccctactctcccaaaatctccaaagcctatcaagtttga 1129
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 270 gctttctggtgcaccagcatgaagacataccgagtgataaaattctgtgagatgtaccga 329
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1130 gctttctggtgcaccagcatgaagacataccgagtgataaaattctgtgagatgtaccga 1189
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 330 cggcggatgctgcacccccccacagacacacccctgcgggtgaggttcaagtgccctga 389
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1190 cggcggatgctgcacccccccacagacacacccctgcgggtgaggttcaagtgccctga 1249
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 390 cggcggatgctgaagagaacatgattctcaacagacctgtgcctgccattcaactg 449
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1250 cggcggatgctgaagagaacatgattctcaacagacctgtgcctgccattcaactg 1309
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 450 tcccgagagaatgacatctttgactcgtgtactacaggaagatgtacgagacatggc 509
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1310 tcccgagagaatgacatctttgactcgtgtactacaggaagatgtacgagacatggc 1369
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 510 a 510
|
Db 1370 a 1370

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Job time: 2470 sec

us-09-461-646-1_copy_667_1176.rng

Tue Aug 21 08:16:51 2001

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2001, 21:26:19 ; Search time 80.25 Seconds
(without alignments)
1203.099 Million cell updates/sec

Title: US-09-461-646-1_COPY_667_1176

Perfect score: 510

Sequence: 1 gcgcctaccactggaaga.....agatgtacggagacatgca 510

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9455562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510	100.0	2075	1	US-08-167-628-1
2	510	100.0	2075	1	US-08-386-680-1
3	510	100.0	2075	1	US-08-459-717-1
4	510	100.0	2075	1	US-08-712-302-1
5	510	100.0	2075	2	US-08-880-031-1
6	510	100.0	2075	3	US-09-097-179-1
7	510	100.0	2075	4	US-09-080-715-1
8	510	100.0	2075	5	PCT-US96-08140-1
9	510	100.0	2998	3	US-09-054-368-1
10	510	100.0	2998	3	US-09-054-274-1
11	510	100.0	2998	4	US-09-056-704-1
12	154	30.2	1128	2	US-08-459-101A-1
13	36	7.1	1158	3	US-08-844-188-45
14	34.2	6.7	293	3	US-08-866-340-13
15	34.2	6.7	293	3	US-09-103-875-17
16	33.2	6.1	15202	3	US-08-922-635-21
17	31	6.1	9757	1	US-08-093-453B-1
18	31	6.1	9759	1	US-08-459-041A-1
19	31	6.1	9759	3	US-08-999-733-1
20	30.8	6.0	1176	2	US-08-387-942C-17
21	30.8	6.0	12588	2	US-08-387-942C-1
22	30.8	6.0	28958	1	US-08-258-261B-6
23	30.8	6.0	28958	1	US-08-456-837-6
24	30.8	6.0	28958	1	US-08-457-342-6
25	30.8	6.0	28958	1	US-08-457-646A-6
26	30.8	6.0	28958	1	US-08-458-076A-6
27	30.8	6.0	28958	1	US-08-764-233A-4

ALIGNMENTS

RESULT 1

US-08-167-628-1

; Sequence 1, Application US/08167628

; Patent No. 5408040

; GENERAL INFORMATION:

; APPLICANT: Grotendorst, Gary R.

; APPLICANT: Bradham Jr., Douglas M.,

; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Spensley Horn Jubas & Lubitz

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/167,628

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/752,427

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Wetherell, Jr. Ph.D., John W.

; REGISTRATION NUMBER: 31,678

; REFERENCE/DOCKET NUMBER: PD-1294

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-455-5100

; TELEFAX: 619-455-5110

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2075 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; CLONE: DB60R32

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 130..1177

; US-08-167-628-1

Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli

us-09-461-646-1_copy_667_1176.rni

Tue Aug 21 08:16:52 2001

REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-386-680-1

Query Match 100.0%; Score 510; DB 1; Length 2075;
Best Local Similarity 100.0%; Pred. No. 9,8e-139; Indels 0; Gaps 0;
Matches 510; Conservative

QY 1 ggggtaccgactgaagacacgtttggccagacaccccaactatgattagagccaactgc 60
Db 667 GCGGCTTACCGACTGGAAGACACGTTTGGCCAGACACCTATGATTAGAGCCAACTGC 726
QY 61 ctggtccagaccagagtgaggcgctgttccaaagacaccccaactatgattagagccaactgc 120
Db 667 GCGGCTTACCGACTGGAAGACACGTTTGGCCAGACACCTATGATTAGAGCCAACTGC 726
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Db 727 CTGCTCCAGACACAGAGTGGAGCGCTTCTTCCAAAGACCTGTGGATGGCATCTCCACC 786
QY 121 cgggttaccgaatgacacgctcctcaggtcaggtagagaagcagagccgctgtgcatgctc 180
Db 787 CCGGTTACCAATGACAAAGCTTCTGCGAGCTAGAGAGCAATTAAGAGGGCAAAAGTGCATCGTACT 906
QY 181 aggccttcggaagctgacccctggaagagagaaattaaagaggcaaaagtgcacccgtact 240
Db 847 AGGCTTCCGAAGCTGACCTGGAAGAGCAATTAAGAGGGCAAAAGTGCATCGTACT 906
QY 241 cccaaatctccaaagcctatcaagtgttgagcttctgtgctgacccagcagcatgaagacacac 300
Db 907 CCCAAATCTCCAAAGCTGACCTGGAAGAGCAATTAAGAGGGCAAAAGTGCATCGTACT 906
QY 301 cggagctaaattctgaggatgtaccgagcggcgatgtgcaccccccacagaaacacc 360
Db 967 CGAGCTAAATTTCTGTGGAGTATGTACCGACGCGGATGCTGACCCCCACAGAACACC 1026
QY 361 accctcgggtgagttcaagtgcctcaggtcaggtcaggtcaggtcaggtcaggtcaggtcaggtc 420
Db 1027 ACCCTGCGGTGGAGTCAAGTGCCTGACGCGGAGGTCATGAAGAGCAATGAAGACATCATCTTC 1086
QY 421 atcaagacctgtgctgcccattacaaactgtcccgagagacaatgacatctttgaatcgctg 480
Db 1087 ATCAAGACCTGTGCTGCCATTACACTGTCGCGGAGACAATGACATCTTTGAATCGCTG 1146
QY 481 tactacaggaagatgtacggagacatggca 510
Db 1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176

RESULT 3
US-08-459-717-1
Sequence 1, Application US/08459717
Patent No. 5770209
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400

Query Match 100.0%; Score 510; DB 1; Length 2075;
Best Local Similarity 100.0%; Pred. No. 9,8e-139; Indels 0; Gaps 0;
Matches 510; Conservative

QY 1 ggggtaccgactgaagacacgtttggccagacaccccaactatgattagagccaactgc 60
Db 667 GCGGCTTACCGACTGGAAGACACGTTTGGCCAGACACCTATGATTAGAGCCAACTGC 726
QY 61 ctggtccagaccagagtgaggcgctgttccaaagacaccccaactatgattagagccaactgc 120
Db 667 GCGGCTTACCGACTGGAAGACACGTTTGGCCAGACACCTATGATTAGAGCCAACTGC 726
QY 727 CTGCTCCAGACACAGAGTGGAGCGCTTCTTCCAAAGACCTGTGGATGGCATCTCCACC 786
Db 727 CTGCTCCAGACACAGAGTGGAGCGCTTCTTCCAAAGACCTGTGGATGGCATCTCCACC 786
QY 121 cgggttaccgaatgacacgctcctcaggtcaggtagagaagcagagccgctgtgcatgctc 180
Db 787 CCGGTTACCAATGACAAAGCTTCTGCGAGCTAGAGAGCAATTAAGAGGGCAAAAGTGCATCGTACT 906
QY 181 aggccttcggaagctgacccctggaagagacattaaagaggcaaaagtgcacccgtact 240
Db 847 AGGCTTCCGAAGCTGACCTGGAAGAGCAATTAAGAGGGCAAAAGTGCATCGTACT 906
QY 241 cccaaatctccaaagcctatcaagtgttgagcttctgtgctgacccagcagcatgaagacacac 300
Db 907 CCCAAATCTCCAAAGCTGACCTGGAAGAGCAATTAAGAGGGCAAAAGTGCATCGTACT 906
QY 301 cggagctaaattctgaggatgtaccgagcggcgatgtgcaccccccacagaaacacc 360
Db 967 CGAGCTAAATTTCTGTGGAGTATGTACCGACGCGGATGCTGACCCCCACAGAACACC 1026
QY 361 accctcgggtgagttcaagtgtcctcaggtcaggtcaggtcaggtcaggtcaggtcaggtcaggtc 420
Db 1027 ACCCTGCGGTGGAGTCAAGTGCCTGACGCGGAGGTCATGAAGAGCAATGAAGACATCATCTTC 1086
QY 421 atcaagacctgtgctgcccattacaaactgtcccgagagacaatgacatctttgaatcgctg 480
Db 1087 ATCAAGACCTGTGCTGCCATTACACTGTCGCGGAGACAATGACATCTTTGAATCGCTG 1146
QY 481 tactacaggaagatgtacggagacatggca 510
Db 1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176

RESULT 2
US-08-386-680-1
Sequence 1, Application US/08386680
Patent No. 5585270
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM: disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,680
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.

CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,717
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/752,427
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-459-717-1

Query Match 100.0%; Score 510; DB 1; Length 2075;
Best Local Similarity 100.0%; Pred. No. 9.8e-139;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttacgcagactggaagacacgcttggcccgagacccaactatgattagagcaactgc 60
Db 667 GCGGCTTACCGACTGGAAGACACGTTTGGCCCGACAGCCAACTATGATTAGAGCCAACCTGC 726

QY 61 ctggtccagaccacagagtgagcctgttccaagacctgtggatggcactctccacc 120
Db 727 CTGGTCCAGACCACAGAGTGGAGCGGCTGTCCAAAGACCTGTGGGATGGCATCTCCACC 786

QY 121 cgggtttaccaatgacaacgcctctcaggtctagagaagcagagccgcctgtgcatggtc 180
Db 787 CGGTTACCAATGACAACGCCTCTCGAGCTAGAGAAGCAGAGCCGCTGTGCATGCTC 846

QY 181 aggccttgcaagctgacctgggaagaaacattaaagaagggaagaaagtgcactc 240
Db 847 AGGCTTGGCAAGCTGACCTGGAAGAAACATTAAAGAAGGGCAAAAAGTGCATCCGTACT 906

QY 241 cccaaatctccaaagcctatcaagtttgagcttcttgctgcaccagcagcatgaagacatac 300
Db 907 CCCAAATCTCCAAAGCTTATCAAGTTTGAGCTTTCGGCTGACACAGCATGAAGACATAC 966

QY 301 cgagctaaattctgtgagtatgtaccagcggccgagctgtgcacccccccacagaaaccacc 360
Db 967 CGAGCTAAATCTCTGGAGTATGTACCGAGCGCGGATGTGACCCCGGACACCAACCCACC 1026

QY 361 accctccgggtgaggttcaagtcacccctgacggcgaggttcattgaagaagaacatgatttc 420
Db 1027 ACCCTCCGGGTGAGGTTCAGAGTCCCTTGACGGGAGGTTCATGAAGAAGAACATGATGTTTC 1086

QY 421 atcaagacctgtgcctgacattacagactgtcccgagagacaataacatcttctgaatgcctg 480
Db 1087 ATCAAGACCTGTGCTGCCATTACAAGTGTCCCGGAGACAATGACATCTTTGAATCGCTG 1146

QY 481 tactacaggaagatgtacgagacatggca 510
Db 1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176

RESULT 4
US-08-712-302-1
Sequence 1, Application US/08712302
Patent No: 5783187
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-712-302-1

Query Match 100.0%; Score 510; DB 1; Length 2075;
Best Local Similarity 100.0%; Pred. No. 9.8e-139;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttacgcagactggaagacacgcttggcccgagacccaactatgattagagcaactgc 60
Db 667 GCGGCTTACCGACTGGAAGACACGTTTGGCCCGACAGCCAACTATGATTAGAGCCAACCTGC 726

QY 61 ctggtccagaccacagagtgagcctgttccaagacctgtggatggcactctccacc 120
Db 727 CTGGTCCAGACCACAGAGTGGAGCGGCTGTCCAAAGACCTGTGGGATGGGCATCTCCACC 786

QY 121 cgggtttaccaatgacaacgcctctcaggtctagagaagcagagccgcctgtgcatggtc 180

NAME/KEY:	CDS	130..1177	DB 2:	Length	2075:	0:
LOCATION:						
US-08-880-031-1						
Query Match	100.0%;	Score 510;	DB 2:	Length	2075:	0:
Best Local Similarity	100.0%;	Prod. No. 9.8e-139;				
Mismatches	0;	Mismatches	0;	Indels	0;	Gaps
Matches	510;	Conservative	0;			
QY	1	cgcggtaccgactgaagacacgcttgcccgagaccacatgattagagccaactgc	726			
DB	667	CGGGCTTACCgactTGAAGACACgCTTGGCCAGACCCAACTATGATTAGAGCCAACCTGC	726			
QY	61	ctggtccagacacagagtggagcgcctgtctccagacccttggatggcatctccacc	120			
DB	667	CGGGCTTACCgactTGAAGACACgCTTGGCCAGACCCAACTATGATTAGAGCCAACCTGC	726			
QY	61	ctggtccagacacagagtggagcgcctgtctccagacccttggatggcatctccacc	120			
DB	727	CTGGTCCAGACCACAGAGTGAGGGCGCTGTCTCCAGACCTGTGGGATGGGCATCTCCACC	786			
QY	121	cgggtattcaatgaacacgcctctcgagcttagaagacgagcgcgcctgtgcattgtc	180			
DB	727	CTGGTCCAGACCACAGAGTGAGGGCGCTGTCTCCAGACCTGTGGGATGGGCATCTCCACC	786			
QY	121	cgggtattcaatgaacacgcctctcgagcttagaagacgagcgcgcctgtgcattgtc	180			
DB	787	CGGGTTACCAATGACACCGCTTCCAGACCTGTGGGATGGGCATCTCCACT	906			
QY	181	agcctctgcgaagctgaacctggaagaaacattaaagaaggcaaaagtgcattccgtact	240			
DB	787	CGGGTTACCAATGACACCGCTTCCAGACCTGTGGGATGGGCATCTCCACT	906			
QY	181	agcctctgcgaagctgaacctggaagaaacattaaagaaggcaaaagtgcattccgtact	240			
DB	847	AGGCGCTTCGGAAGCTGACCTGGGAAGAGAACATTAAGAAGGGCAAAAGTGATCCGCTACT	300			
QY	241	cccaaaattccaaagcctatcaagtgttagctttcttggtgtgaccagcatgaagacatac	366			
DB	847	AGGCGCTTCGGAAGCTGACCTGGGAAGAGAACATTAAGAAGGGCAAAAGTGATCCGCTACT	300			
QY	241	cccaaaattccaaagcctatcaagtgttagctttcttggtgtgaccagcatgaagacatac	366			
DB	907	CCCAAAATCTCCAAAGCCTATCAAGTTTGAGCTTTCTGGCTGACACGAGCATGAAGACATATC	966			
QY	301	cgagctaaattctgtggagtgtaccgagccgctgtgaccgccacacagaaccacc	360			
DB	907	CCCAAAATCTCCAAAGCCTATCAAGTTTGAGCTTTCTGGCTGACACGAGCATGAAGACATATC	966			
QY	301	cgagctaaattctgtggagtgtaccgagccgctgtgaccgccacacagaaccacc	360			
DB	967	CGAGCTAAATCTGTGGAGTATGTACGACGGCCGATGCTGCACCCCCACAGAACCATC	1026			
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DB	967	CGAGCTAAATCTGTGGAGTATGTACGACGGCCGATGCTGCACCCCCACAGAACCATC	1026			
QY	361	accctgcgcgtgagttcaagtgccctgacgcgcgaggtcatgaagaagaacatgattc	420			
DB	1027	ACCTGTGCCGTGGAGTTCAGTGCCTCAGCGGAGTCAATGAAGAAGAACATGATGTTTC	1086			
QY	480	acctgtgccgtggagttcaagtgccctgacgcgcgaggtcatgaagaagaacatgattc	480			
DB	1027	ACCTGTGCCGTGGAGTTCAGTGCCTCAGCGGAGTCAATGAAGAAGAACATGATGTTTC	1086			
QY	480	acctgtgccgtggagttcaagtgccctgacgcgcgaggtcatgaagaagaacatgattc	480			
DB	1027	ACCTGTGCCGTGGAGTTCAGTGCCTCAGCGGAGTCAATGAAGAAGAACATGATGTTTC	1086			
QY	421	atcaagacatgtgctgcattacaaactgtcccgagacaagaatgacattttgaatcgctg	1146			
DB	1027	ACCTGTGCCGTGGAGTTCAGTGCCTCAGCGGAGTCAATGAAGAAGAACATGATGTTTC	1086			
QY	421	atcaagacatgtgctgcattacaaactgtcccgagacaagaatgacattttgaatcgctg	1146			
DB	1087	ATCAAGACCTGTGCCCTGCCATTACAATTCACAACTGTCCCGGAGNACNATGACATCTTTTGAAATCGCTG	1146			
QY	481	tactacagaaagatatacggagacatggca	510			
DB	1087	ATCAAGACCTGTGCCCTGCCATTACAATTCACAACTGTCCCGGAGNACNATGACATCTTTTGAAATCGCTG	1146			
QY	481	tactacagaaagatatacggagacatggca	510			
DB	1147	TACTACAGGAAGATGTACGGAGATGGCA	1176			

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6 RESULT
US-09-097-179-1 Application US/09097179
; Sequence 1, Application
; Patent NO. 6149916
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS: Horn Jubas & Lubitz
; ADDRESSEE: Spensley Executive Square, Suite 1400
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097.179
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,680

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847 AGGCTTGGGAAGCTGACCTGGAAGAGAACATTAAAGAGGGCAAAAAGTGCAATCCGTACT 906
241 cccaaatctccaaagcctatacaagttagctttctggctgcaccagatgaagacatac 300
907 CCCAATAATCTCCAAGCTATCAAGTTTGAGCTTTCTGGCTGCACAGCATGAAGACATAC 966
301 cgagctaaattctgtgagtatgtaccagagcgccgatctgaccccccacagaaccacc 360
967 CGAGCTAAATTCGTGAGGTATGTACCGACGGCCGATGCTGCACCCCCACAGACCACC 1026
361 accctgcgggtggagttcaagtgcctctgacggcgaggtcatgaagaagaacatgattc 420
1027 ACCCTGCCGGTGGAGTTCAGTGCCTTGACGGCGAGGTGATGAAGAAGAACATGATGTTTC 1086
421 atcaagacctgtgcctgcccattcaactgtcccgagagacaatacactcttgtaactcgtg 480
1087 ATCAAGACCTGTGCTGCCCTTACACTGTGCCGGAGACAATGACATCTTTGAATCGCTG 1146
481 tactacaggaagtgtacggagacatggca 510
1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176

RESULT 5
US-08-880-031-1
; Sequence 1, Application US/08880031
; Patent No. 5916756
; GENERAL INFORMATION:
; APPLICANT: Grotdorst, Gary R.
; APPLICANT: Bradham Jr, Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/880,031
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/167,628
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph. D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5110
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2075 base pairs
; TYPE: nucleic acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: DB60H32
; FEATURE

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; FILING DATE: 10-FEB-1995
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2075 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: DB60R32
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 130..1177
; US-09-097-179-1

Query Match 100.0%; Score 510; DB 3; Length 2075;
Best Local Similarity 100.0%; Pred. No. 9.8e-139;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttaccgactggaagacacgctgttccaaagacctgtgggagtgccatccacc 60
DB 667 GCGGCTTACCAGCTGGAAGACACGCTTTGGCCACACCACTATGATTAGAGCCAACTGC 726
QY 61 ctggtccagaccagagtgagcgctgttccaaagacctgtgggagtgccatccacc 120
DB 727 CTGCTCCAGACCACAGAGTGAGGCGCTTCTCCAAAGACCTGTGGGATGGGCATCTCCACC 786
QY 121 cgggttaccatgacaacgcctctcaggtcagagcagagcagccgctgtgcatggtc 180
DB 787 CCGGTTTACCAGCTGGAAGACACGCTTCTCCAAAGACCTGTGGGATGGGCATCTCCACC 846
QY 181 agccttcggaagctgacacgctcctcaggtcagagcagagcagagcagagcagagcagac 300
DB 847 AGGCTTTCGAAGCTGACCTGGAAGACACATTAAGAAGGGCAAAAGTGCATCCGTACT 906
QY 241 cccaaatctccaaagcctatcaagtttgagcttctgtgctgaccagcagcagacacacac 480
DB 907 CCCAAATCTCCAAAGCTATCAAGTTTGGCTTCTGGCTGCACCCACAGACATAC 966
QY 301 cgagctaaattctgtgagtatgtaccagcgcgctgtgctgaccagcagcagacacacac 360
DB 967 CGAGCTAAATCTGTGAGTATGTACGACGCGGCTGTGCTGCACCCACAGAACACAC 1026
QY 361 accctgcggtgaggttcaagtcgctcagcgcgagtgatcatgaagaagaacatgatgttc 420
DB 1027 ACCCTGCGGTGGAGTTCAAGTGCCTGACGGGAGGTGATGAAGAAGACATGATGTC 1086
QY 421 atcaagacctgtgctgctcattcaactgtcccgagagacatgacatctttgaaatcgtg 480
DB 1087 ATCAAGACCTGTGCTGCTCATTCAACTGTCGCGGAGACAAATGACATCTTTGAATCGCTG 1146
QY 481 tactacaggaagatgtacgagacatggca 510
DB 1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176

RESULT 7
US-09-080-715-1
; Sequence 1, Application US/09080715
; Patent No. 6190884
; GENERAL INFORMATION:

; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2075 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: DB60R32
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 130..1177
; US-09-080-715-1

Query Match 100.0%; Score 510; DB 4; Length 2075;
Best Local Similarity 100.0%; Pred. No. 9.8e-139;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttaccgactggaagacacgctgttccaaagacctgtgggagtgccatccacc 60
DB 667 GCGGCTTACCAGCTGGAAGACACGCTTTGGCCACACCACTATGATTAGAGCCAACTGC 726
QY 61 ctggtccagaccagagtgagcgctgttccaaagacctgtgggagtgccatccacc 120
DB 727 CTGCTCCAGACCACAGAGTGAGGCGCTTCTCCAAAGACCTGTGGGATGGGCATCTCCACC 786
QY 121 cgggttaccatgacaacgcctcctcaggtcagagcagagcagagcagagcagagcagagcagac 180
DB 787 CCGGTTTACCAGCTGGAAGACACGCTTCTCCAAAGACCTGTGGGATGGGCATCTCCACC 846
QY 181 agccttcggaagctgacacgctcctcaggtcagagcagagcagagcagagcagagcagac 240
DB 847 AGGCTTTCGAAGCTGACCTGGAAGACACATTAAGAAGGGCAAAAGTGCATCCGTACT 906
QY 241 cccaaatctccaaagcctatcaagtttgagcttctgtgctgaccagcagcagacacacac 300
DB 907 CCCAAATCTCCAAAGCTATCAAGTTTGGCTTCTGGCTGCACCCACAGACATAC 966
QY 301 cgagctaaattctgtgagtatgtaccagcgcgctgtgctgaccagcagcagacacacac 360
DB 967 CGAGCTAAATCTGTGAGTATGTACGACGCGGCTGTGCTGCACCCACAGAACACAC 1026
QY 361 accctgcggtgaggttcaagtcgctcagcgcgagtgatcatgaagaagaacatgatgttc 420
DB 1027 ACCCTGCGGTGGAGTTCAAGTGCCTGACGGGAGGTGATGAAGAAGACATGATGTC 1086
QY 421 atcaagacctgtgctgctcattcaactgtcccgagagacatgacatctttgaaatcgtg 480
DB 1087 ATCAAGACCTGTGCTGCTCATTCAACTGTCGCGGAGACAAATGACATCTTTGAATCGCTG 1146
QY 481 tactacaggaagatgtacgagacatggca 510
DB 1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176

Qy	181	aggccttggaagctgacctggagaagaacattaagaaggcgaagaagtgcacgtact	240
Db	1742	aggccttggaagctgacctggagaagaacattaagaaggcgaagaagtgcacgtact	1801
Qy	241	cccaaaatctcaagcctataagtttagctttctggctgcacacgcatgaagacatac	300
Db	1802	cccaaaatctcaagcctataagtttagctttctggctgcacacgcatgaagacatac	1861
Qy	301	cgaqctaaaattctgtggatgtaccacagcgcatgtcacccccacagacacc	360
Db	1862	cgaqctaaaattctgtggatgtaccacagcgcatgtcacccccacagacacc	1921
Qy	361	acccctgcggtggagtccaagtgcctgacgcgaggtcactgaagaagaacatgattc	420
Db	1922	acccctgcggtggagtccaagtgcctgacgcgaggtcactgaagaagaacatgattc	1981
Qy	421	atcaagacctgtgcctgccattacaactgtccggagacaatgcattttgaatcgctg	480
Db	1982	atcaagacctgtgcctgccattacaactgtccggagacaatgcattttgaatcgctg	2041
Qy	481	tactacaggaagatgtacggagacatggca	510
Db	2042	tactacaggaagatgtacggagacatggca	2071

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RESULT 10
US-09-054-274-1
; Sequence 1, Application US/09054274
; Patent No. 6150101
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham, Jr., Douglass M.
; TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION
; TITLE OF INVENTION: THAT ALTERS CONNECTIVE TISSUE GROWTH
; TITLE OF INVENTION: FACTOR EXPRESSION (Amended)
; FILE REFERENCE: 07414/003004
; CURRENT APPLICATION NUMBER: US/09/054,274
; CURRENT FILING DATE: 1998-04-02
; EARLIER APPLICATION NUMBER: 08/386,680
; EARLIER FILING DATE: 1995-02-10
; EARLIER APPLICATION NUMBER: 08/459,717
; EARLIER FILING DATE: 1995-06-02
; EARLIER APPLICATION NUMBER: 08/167,628
; EARLIER FILING DATE: 1993-12-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2970
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1025)...(2074)
US-09-054-274-1

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Qy	181	aggccttgcaagctgacctggaagaacatttaagaaggccaataatgcatccgtact	240
Db	1742	aggccttgcaagctgacctggaagaacatttaagaaggccaataatgcatccgtact	1801
Qy	241	cccaaaatctccaagcctatcaagtgttgagctttctggtgcaccagcatgaagacatac	300
Db	1802	cccaaaatctccaagcctatcaagtgttgagctttctggtgcaccagcatgaagacatac	1861
Qy	301	cgagctaaattctgtgagtatgtaccgacgcccgcgatgctgcacccccacagaaccacc	360
Db	1862	cgagctaaattctgtgagtatgtaccgacgcccgcgatgctgcacccccacagaaccacc	1921
Qy	361	acctgcgggtggagttccaagtgcctgcacgcgagggtcattgaagaagaacatgatgttc	420
Db	1922	acctgcgggtggagttccaagtgcctgcacgcgagggtcattgaagaagaacatgatgttc	1981
Qy	421	atcaagacctgtccctgccattacaactgtcccgagagacaatgacatctttgaaatcgctg	480
Db	1982	atcaagacctgtccctgccattacaactgtcccgagagacaatgacatctttgaaatcgctg	2041
Qy	481	tactacaggaagatgtacggagacatggca	510
Db	2042	tactacaggaagatgtacggagacatggca	2071
RESULT 11			
US-09-056-704-1			
; Sequence 1, Application US/09056704			
; Patent No. 6232064			
; GENERAL INFORMATION:			
; APPLICANT: University of South Florida			
; APPLICANT: Grotendorst, Gary R.			
; APPLICANT: Bradham, Jr., Douglass M.			
; TITLE OF INVENTION: METHODS OF DIAGNOSING A PATHOLOGY			
; TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE			
; TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE			
; TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)			
; FILE REFERENCE: 07414/003002			
; CURRENT APPLICATION NUMBER: US/09/056,704			
; CURRENT FILING DATE: 1998-03-03			
; EARLIER APPLICATION NUMBER: 08/386,680			
; EARLIER FILING DATE: 1995-02-10			
; EARLIER APPLICATION NUMBER: 08/459,717			
; EARLIER FILING DATE: 1995-06-02			
; EARLIER APPLICATION NUMBER: 08/167,628			
; EARLIER FILING DATE: 1993-12-14			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 2970			
; TYPE: DNA			
; ORGANISM: Homo Sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1025) ... (2074)			
US-09-056-704-1			

us-09-461-646-1_copy_667_1176.rni

Tue Aug 21 08:16:52 2001

Best Local Similarity 61.0%; Pred. No. 1.3e-35; Mismatches 160; Indels 0; Gaps 0; Matches 250; Conservative

Db 1682 cgggttaccaatgacaagcctcctcaggttagaagagagagcccgctgcatggtc 1741
Qy 181 aggccttgaaagctgacctgaaagagacattaaagagggaagggcaaaagtgcacgtact 240
Db 1742 aggccttgaaagctgacctgaaagagacattaaagagggaagggcaaaagtgcacgtact 1801
Qy 241 ccaaaatctccaagcctatcaagtttgagcttctgctgacccagcatgaagacatac 300
Db 1802 ccaaaatctccaagcctatcaagtttgagcttctgctgacccagcatgaagacatac 1861
Qy 301 cgaagctaaatctgagatgattgacccagggccgagctgaccccccacagaaacacc 360
Db 1862 cgaagctaaatctgagatgattgacccagggccgagctgaccccccacagaaacacc 1921
Qy 361 accctgcggtgaggttcaagtgccctgacggaggtcatgaagaagacatgatgttc 420
Db 1922 accctgcggtgaggttcaagtgccctgacggaggtcatgaagaagacatgatgttc 1981
Qy 421 atcaagacctgctgctgccattacaactgtcccgagagacatacattttgaatcgctg 480
Db 1982 atcaagacctgctgctgccattacaactgtcccgagagacatacattttgaatcgctg 2041
Qy 481 tactacaggaagatgacgagagacatgca 510
Db 2042 tactacaggaagatgacgagagacatgca 2071

RESULT 12
US-08-459-101A-1
; Sequence 1, Application US/08459101A
; Patent No. 5945300
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Connective Tissue Growth Factor-2
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,101A
; FILING DATE: June 2, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07736
; FILING DATE: 12 JUL 94
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1128 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-459-101A-1

Query Match 30.2%; Score 154; DB 2; Length 1128;

RESULT 13
US-08-844-188-45
; Sequence 45, Application US/08844188
; Patent No. 6127180
; GENERAL INFORMATION:
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Knuth, Mark
; APPLICANT: Pollard, Michael R.
; APPLICANT: Cardineau, Guy
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Pesticidal Toxins
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,188
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/633,993
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-703C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 45:

Qy 55 aactgcctggtccagaccacacagagagcgcctgttcccaagacccctgtggtggtggtc 114
Db 685 AAATGATATTGTTCAAAACAACTTCATGTCCTCCAGTGCTCAAAGACCTGTGGAACCTGTG 744
Qy 115 tcaccccggtttaccatgacacgcctcctcgcgggctagagaagagagagcccgctgtgc 174
Db 745 TCACACAGAGTTACCAATGACAACCTGAGTCCGCTGTGAAAGAGAAACCCGGATTGT 804
Qy 175 atggtcagccttggaagctgacctggaagagacattaaagagggaagggcaaaagtgcac 234
Db 805 GAGGTGCGGCTTGTGGACAGCGCTGTACACGCTGAAAAGGGCAGAAAATGCGC 864
Qy 235 cgtactcccaaatctcccaagcctcctcgaagttgagcttctggtgctgacccagcatgaa 294
Db 865 AGACCAAGAAATCCCGAACGATGAGTTTACTTACGCTGGATGTTTGTGAGTGTGAAG 924
Qy 295 acatccagcgtataattctgtgagtagtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 354
Db 925 AAATACCGCGCCCAAGTACTCGGTTCTCGTGGACGGCCGATGCTGCACGCCCCAGCTG 984
Qy 355 accaccacccctgcgggtgaggttcaagtgccctgacggaggtcatgaagaagacatg 414
Db 985 ACCAGGACTGTGAAGATGCGGTTCCCTCGGAAAGATGGGGAGACATTTTCCCAAGAACGTC 1044
Qy 415 atgttcacaaagacccctgctgctgacattacaactgtcccgaggagacatga 464
Db 1045 ATGATGATCCAGTCTCTCAATGCACTACACTGCGCCGATGCCAARGA 1094

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1158 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-844-188-45

Query Match          7.1%; Score 36; DB 3; Length 1158;
Best Local Similarity 48.1%; Pred. No. 0.21;
Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 54 caactgctgttcagaccacagatgagcgctgttccaagacctgtggtatgggcat 113
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Db 945 CACCTCCCTCGAGCTGACCGCTACACCGCAGCGAGATCAAGATCATGACATCGAGAC 1004

QY 114 ctccaccgggttaccaatgacaacgctcctcgcaggctagagaagcagcgccctgtg 173
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Db 1005 CTCGACCGACGACCTTACACCTCCTACCTCCTACCTCCTACCTCCTACCTCCTACCT 1064

QY 174 catggtcagcgcttgcgaagctgacccctcgcaggatgaagaaagggcaaaagtgc 233
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1065 GCTGACCAACCACTCTTACAGAGGTTGGAGGATCACCAGATCCCGAAGCACACCT 1124

QY 234 ccgtactcccaaatctcccaagctatcaagt 265
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Db 1125 CATCAAGCTCAAGAAGCACTACTTCAAGAAGT 1156

RESULT 14
US-08-866-340-13/c
; Sequence 13, Application US/08866340
; Patent No. 6020318
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
; TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,340
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Keown, Wayne A.
; REGISTRATION NUMBER: 33,923
; REFERENCE/DOCKET NUMBER: 106.101.187
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-866-340-13
Query Match          6.7%; Score 34.2; DB 3; Length 293;
Best Local Similarity 60.0%; Pred. No. 0.42;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 123 ggttaccaatgacaacgcctcctcgcaggctagagaagcagagccgctgtgcatggctcag 182
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Db 249 GGTTCACAGTCACATGGCCTTCTGCAAGCCTGCTGAGAATTCACCACGAGAGCCCCGTCAG 190

QY 183 gccttgcaagctgacccctcgcaggatgaagaaacattaaaga 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 CCCCCAGGAGGAGAACATGAAGGCCCTTTCAGA 155

RESULT 15
US-09-103-875-17/c
; Sequence 17, Application US/09103875A
; Patent No. 6221849
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: 106101.194
; CURRENT APPLICATION NUMBER: US/09/103,875A
; CURRENT FILING DATE: 1998-06-24
; EARLIER APPLICATION NUMBER: 60/069,865
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 08/866,340
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-103-875-17

Query Match          6.7%; Score 34.2; DB 4; Length 293;
Best Local Similarity 60.0%; Pred. No. 0.42;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Db 249 GGTTCACAGTCACATGGCCTTCTGCAAGCCTGCTGAGAATTCACCACGAGAGCCCCGTCAG 190

QY 183 gccttgcaagctgacccctcgcaggatgaagaaacattaaaga 217
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Db 189 CCCCCAGGAGGAGAACATGAAGGCCCTTTCAGA 155

Search completed: August 20, 2001, 22:08:26
Job time: 2527 sec
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us-09-461-646-1_copy_667_1176.rni

Tue Aug 21 08:16:52 2001

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2001, 21:23:54 ; Search time 1173.23 Seconds
(without alignments)
4109.131 Million cell updates/sec

Title: US-09-461-646-1_COPY_667_1176

Perfect score: 510

Sequence: 1 gcggctaccgactggaaga.....agatgtacggagacatggca 510

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST:*

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2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
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8: gb_est8:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SOURCE      human..
ORGANISM    Homo sapiens
LOCUS       602318833F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4423185 5',
DEFINITION mRNA sequence.
REFERENCE   1 (bases 1 to 854)
AUTHORS    Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
            Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
            Isogai, T.
TITLE      HRI human cDNA project
COMMENT     Unpublished (2000)
            Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@hri.co.jp
            HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES   Location/Qualifiers
            1..854
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="HEMBAL1003198"
            /dev_stage="embryo, 10 weeks"
            /note="Vector: pME18SFL3"
BASE COUNT 204 a 277 c 225 g 144 t
ORIGIN
Query Match      90.6%; Score 462.2; DB 107; Length 854;
Best Local Similarity 97.1%; Pred. No. 9.2e-125;
Matches 470; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 gcggctaccgactgaagacacgcttggccagaccacccaactatgattagagcaactgc 60
DB 300 CGCGCTTACCGACTGGAAGACAGCGTGTGGCCAGACCCCACTATGATTAGAGCAACTGCG 359
QY 61 ctggtccagaccacagagtgagcgctgttccaaagacctgtggatgggcatctccacc 120
DB 360 CTGCTCCAGACACACAGAGTGGAGCGCTGTTCACAGACCTGTGGATGGCATCTCCACC 419
QY 121 cgggttaccatgacacgctctcctgcaggctagagaagacagagccgctgtgatgttc 180
DB 420 CGGGTTACCAATGACACAGCGCTCTCTGCAGGCTAGAGAAGCAGAGCGCGCTGTGCATGTC 479
QY 181 aggccttcggaagctgacctgggaagagacattaaagaggcaaaaagtgcacccgtact 240
DB 480 AGGCCTTTCGAAGCTGACCTGGGAAGAGAATTAAGAAGGGCAAAAGTGCATCGCTACT 539
QY 241 cccaaatctccagcctatcaagttagcttcttggctgaccagcagatgaagacatac 300
DB 540 CCCAAATCTCCAGCCTATCAAGTTTGTGCTTCTGCCTGCACCATGATGAAGACATAC 599
QY 301 cgagctaaattctgtggagtgtgtaccagacggcgatgtgtgaccccccacagacccacc 360
DB 600 CGAGCTAAATTTGTGGAGTATGTACCGACGGCCGATGTCTGACCCCCACAGAACCA 659
QY 361 acctgcgggtgagttcaagtgcctgacgagcaggtcatgaagaagaacatgatgttc 420
DB 660 ACCTTGCCTGGTGGAGTTCAAGTGCCTGACGCGGANGTGCATGAAGAAGAAGATGATGTC 719
QY 421 atcaagacctgtgctgcatataactgtcccgagacacatgacatcttttgaatcgtg 480
DB 720 ATCAAGACCTGTGCTGCTATACAACTGTCCCGGAGAGCAATGACATCTTTGAATCGTTG 779
QY 481 tact 484
DB 780 TACT 783

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RESULT 3

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BGI16765      963 bp      mRNA      EST      30-JAN-2001
LOCUS       602318833F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4423185 5',
DEFINITION mRNA sequence.
ACCESSION   BGI16765
VERSION     BGI16765.1
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 963)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10165 row: a column: 10
            High quality sequence stop: 659.
            Location/Qualifiers
            1..963
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="NIH_MGC_88"
            /tissue_type="duodenal adenocarcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: small intestine; Vector: pCMV-SPORT6;
            Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
            oligo-dr primed. Average insert size 1.767 kb. Library
            enriched for full-length clones and constructed by Life
            Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 236 a 244 c 262 g 221 t
ORIGIN
Query Match      88.8%; Score 453; DB 174; Length 963;
Best Local Similarity 99.8%; Pred. No. 4.7e-122;
Matches 464; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 47 ttagagccaactgcctggtccagaccacagagtgagc-gcctgttccaagacctgtggg 105
DB 1 TTAGAGCCAACCTGCCGTGTCAGACACACAGTGGAGCGCGCTGTTCAGAACCTGTGGG 60
QY 106 atgggcatctccacccgggttaccatgacaacgctcctgcaggctagagaagcagagc 165
DB 61 ATGGGCATCTCCACCGGGTTACCAATGACACGCCCTCTCTGCAGGCTAGAGAAGCAGAGC 120
QY 166 cgcctgtgcatggtcaggccttgcgaagctgacctggaagagaacattaaagaaggcaaa 225
DB 121 GCCTGTGCTATGGTTCAGSCCTTGCGAAGCTGACCTGGAAGAGAACATTAAGAAGGCCAAA 180
QY 226 aagtgcattccgtactcccaaaatctccaaagctatcaagttgagcttttgcctgcacc 285
DB 181 AAGTGCATCCGTACTCCCAAAATCTCCAAAGCTATCAAGTTTGAGCTTTCTGCTGCACC 240
QY 286 accatgaagacataccagctgctaaattctgtggagtgtatgtaccagcgccatgtcacc 345
DB 241 ACATGAAGACATACCGAGCTAAATTTCTGTGAGTATGTACCGACGCCGCTGTCGCC 300
QY 346 cccacagaaacacacacccctccggtgagttcaagttccctgacgagcgaggtcatgaag 405
DB 301 CCCCACAGAACCAACCAACCCCTGCCGTGGAGTTCAAGTCCCTGACGCGGAGTCAATGAAG 360

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QY 406 aagaacatgatgttcatacaagacctgtgcctgcattacaaactgtcccgagacaatgac 465
|||||
Db 361 AAGAACATGATGTTTCATCAAGAGCTGTGCTGCATTACAACTGCTCCGGAGACAATGAC 420
|||||
QY 466 atcttgaatcgtgtactacaagaagatgtacgagacatggca 510
|||||
Db 421 ATCTTTGAATCGCTGTACTACAGAAGATGTACGGAGACATGGCA 465
|||||

RESULT 4
LOCUS AW742404 678 bp mRNA EST 07-SEP-2000
DEFINITION up56f10.y1 Soares_mouse_NMIE Mus musculus cDNA clone IMAGE:2780107
5' similar to gb:M80263 Mouse mRNA sequence (MOUSE):..
ACCESSION AW742404
VERSION AW742404.1 GI:7654192
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 678)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -4ORP from Gibco
High quality sequence stop: 471.
FEATURES
Location/Qualifiers
1..678
/organism="Mus musculus"
/strain="C3H x 101 (F1 stock)"
/db_xref="taxon:10090"
/clone="IMAGE:2780107"
/clone_lib="Soares_mouse_NMIE"
/sex="male"
/dev_stage="newborn"
/lab_host="DH10B"
/notes="Organ: Inner ear, 170 pooled; Vector: pT73D-Pac;
Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed
with a Not I - oligo(dT) primer [5',
TGTTCACATCAGTGAAGTGGAGCGCGGCGACACTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
is normalized, and was constructed and donated by Bento
Soares and M.Fatima Ronaldo (University of Iowa) and R.
Hardisty, A. Varela-Carver, P. Mburu and S.D.M. Brown (MRC
UK Mouse Genome Centre and Mammalian Genetics Unit,
Harwell, UK)."
BASE COUNT 187 a 173 c 172 g 146 t
ORIGIN

Query Match 84.7%; Score 432.2; DB 120; Length 678;
Best Local Similarity 90.6%; Pred. No. 5.4e-116;
Matches 461; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 gcgcttaccgactgaagacgtttggccagaccacccaactatgattagcaactgc 60
|||||
Db 57 GCGCTTACCGACTGGAAGACACATTGGCCCGACACCAACTATGATGCGGCAACTGC 116
|||||
QY 61 ctggtccagaccacagtagtgagcgctgttccaagacctgtggatggcgatctccacc 120
|||||
Db 117 CTGGTCAGACACAGATGGCGGCTGTCTTAAGACCTGTGGAATGGGCATCTCCACC 176
|||||
QY 121 cgggttaccaatgacaacgcctcctcaggtctagagaagcagcgccctgtgcatggtc 180
|||||
```

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Db 177 CGAGTTTACCAGTACAAATACCTTCTGCAGACTGGAGAGAGAGCCCGCTTGCATGGTC 236
QY 181 aggccttgcgaagctgacctgggaagaaacattaaagaagggaacaaagtgcataccgtact 240
|||||
Db 237 AGGCCCTGCGNAGCTGACCTGGAGAAAACATTAAAGAGGGCAAAAAGTGCATCCGGACA 296
|||||
QY 241 cccaaaatctccaaagcctatacaagtttgagcttctgtgcaccagcatgaagacatac 300
|||||
Db 297 CCTAAAATCGCCAAAGCCTGTCAAGTTTGTGCTGTCACCCAGTGTGAAGACATAC 356
|||||
QY 301 cgagctaaattctgtgagatgtaccgacgagccgagatgtgcacccccacagaacacc 360
|||||
Db 357 AGGCTTAAGTTCTGCGGGGTGTGCACAGACGGCGCTGCTGCACACCGCACAGAACCAACC 416
|||||
QY 361 accctgcggtggaggttcaagtgccctgacggcgaggtcattcatgaagaagacatgatttc 420
|||||
Db 417 ACTCTGCCAGTGGAGTTCAAAATGCCCGATGGCGAGATCATGAAAAGAATATGATGTTTC 476
|||||
QY 421 atcaagacctgtgcctgccattacaactgtcccgagagacaatgacatctttgaatcgctg 480
|||||
Db 477 ATCAAGACCTGTGCTGCCATTACAACCTGTCTGGGACAAATGACATCTTTGAGTCCTCG 536
|||||
QY 481 tactacaaggaagtgtacggagacatggc 509
|||||
Db 537 TACTACAGGAAGATGTACCGAGACATGGC 565
|||||

RESULT 5
AA187390 487 bp mRNA EST 10-MAR-1998
LOCUS zp70a06.r1 stratagene endothelial cell 937223 Homo sapiens cDNA
DEFINITION clone IMAGE:625522 5' similar to gb:M92934 CONNECTIVE TISSUE GROWTH
FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AA187390
VERSION AA187390.1 GI:1773616
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Hallier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 862 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 340.
FEATURES
Location/Qualifiers
1..487
/organism="Homo sapiens"
/db_xref="GDB:5047676"
/db_xref="taxon:9606"
/clone="IMAGE:625522"
/clone_lib="Stratagene endothelial cell 937223"
/dev_stage="umbilical vein, 1 passage"
/lab_host="SOLR (kanamycin resistant)"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Umbilical vein endothelial cells, passaged once. Average
Insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3'"
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was primed with a NotI-oligo(GT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 179 a 272 c 272 g 154 t 2 others
ORIGIN

Query Match 80.4%; Score 410.4; DB 106; Length 879;
Best Local Similarity 98.8%; Pred. No. 1.9e-109;
Matches 421; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 gcggcttaccgactggaagacacagctgttggccagaccccaactatgattagagcccaactgac 60
Db 453 GCGGCTTACCGACTGGGAAGACACGCTTTGGCCCGACAGCCCACTATGATTAGAGCCCACTGC 512

QY 61 ctgtccagacacagagtgagcgctgttccaaagacctgtgggtggtggtggtggtggtggtggt 120
Db 513 CTGTGTCAGACACAGAGTGGAGCGCTGTTCAGAGACCTGTGGGATGGGCACTCTCCACC 572

QY 121 cgggttaccatgacacgctcctgcaggtagagagagagagagagagagagagagagagagagag 180
Db 573 CGGGTTACCAATACAGCGCTCTCGAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 632

QY 181 agcgttcgagctgagctgag 240
Db 633 AGGCGCTTGGGAATGAG 692

QY 241 cccaaatctccaaagcctcatcaagttgaggttgcaggttgcaggttgcaggttgcaggttgcag 300
Db 693 CCCAAATCTCCAAAGCTATCAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGA 752

QY 301 cagagtaattctgtggagatgtaccagcgagagagagagagagagagagagagagagagagagag 360
Db 753 CGAGCTAAATCTGTGGAGTATGTACCGAGCGGCGATGTCACCGCGGCGGCGGCGGCGGCGGCG 812

QY 361 a-ccttcgaggtgaggttcaagtgccctgagcgaggtgaggtgaggtgaggtgaggtgaggtg 419
Db 813 ACCCTGCGGGTGGAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 872

QY 420 catcaa 425
Db 873 YATCAA 878

RESULT 7
AA221075 696 bp mRNA EST 12-FEB-1997
LOCUS mv75c04.r1 Soares mouse 3NME12 5 Mus musculus cDNA clone
DEFINITION IMAGE:660870 5' similar to gb:M70641 Mouse FISP-12 protein (MOUSE); mRNA sequence.

ACCESSION AA221075
VERSION AA221075.1 GI:1840244
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 696)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project

BASE COUNT 133 a 134 c 121 g 95 t 4 others
ORIGIN

Query Match 80.5%; Score 410.4; DB 3; Length 487;
Best Local Similarity 97.7%; Pred. No. 1.2e-109;
Matches 477; Conservative 0; Mismatches 5; Indels 6; Gaps 6;

QY 20 acagcttggccagaccacacactgattagagcccaactgctgttcagagaccacagagt 79
Db 1 ACAGCTTGGCCCGACACCACTATGATTAGAGCCCACTGCTGTGTCAGACACAGAGT 60

QY 80 ggaagcctgttccagagacactgagtgagctccaccggtgttaccacacacagc 139
Db 61 GAGCGGCTTCTCCAGACCTGTGGAGTGGGATCTCCACCGGTTACCAATGACACAG 120

QY 140 cctcctcaggttagaagaagacagagcgcc-tgtcatggtcagggccttgcaagctaac 198
Db 121 CCTCTCGAGCTAGAGAAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 179

QY 199 ctggaagagacattagaagagggcaaaagtcatcgtactctccaaatctccagcct 258
Db 180 CTGGAAGAGAACATTAAGAGAGGGCAAAAGTGCATCCGTAATCCCAAAATCTCCAAAGCCT 239

QY 259 atcaagttgagcttctggtgcagcagcagcagcagcagcagcagcagcagcagcagcagcag 318
Db 240 ATCAAGTTTGAGCTTCTGGCTGCACACAGCATGAAGACATACCGAGCTAAATTTCTGTGGA 299

QY 319 gtatgacagcagg-cgatgctgaccccccacagacacacacacacacacacacacacacacac 376
Db 300 GTATGTACCGACGGCCGATGCTGCACCCCGCCACAGACACACACACACACACACACACAC 359

QY 377 tcaagtgcctgacggcg-aggtcatgagaagacatgatgttcatcaagacctgtgccc 435
Db 360 TCAAGTGCCTGACCGCGGAGGTCTATGAAGAAGACATGTTTCATCAAGACCTGTGCC 419

QY 436 tgccattacaac-tgtcccgagacacatgacatcttgaatcgtgactacagagagat 494
Db 420 TGCCATTACAACCTTGTCCCGGAGACAATGACATCTTTGAATCGCTGTACTACAGAGAGAT 479

QY 495 gtacgag 502
Db 480 GTACGGAG 487

RESULT 6
AL547439 879 bp mRNA EST 16-FEB-2001
LOCUS AL547439 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1011YE17 5
DEFINITION prime, mRNA sequence.

ACCESSION AL547439
VERSION AL547439.1 GI:12881511
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 879)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CS0D1011YE17"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA source

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:406718
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 499.

FEATURES

SOURCE

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:660870"
/clone_img="Soares mouse"
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/dev_stages="12.5dpc total"
/lab_host="T4H10A"
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/a/mosoc- enibp
/note=Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCGAGTGGAGCGCGCCTATTTTTTTTTTTTTT
3'], on total mouse RNA [provided by Minoru Ko, Wayne
State Univ.]; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library went through one round of normalization, and was
constructed by Hento Soares and M. Fatima Bonaldo.
174 c 169 g 152 t 1 others

	BASE COUNT	COUNT	ORIGIN
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4	0.000	0.000	0.000
5	0.000	0.000	0.000
6	0.000	0.000	0.000
7	0.000	0.000	0.000
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10	0.000	0.000	0.000
11	0.000	0.000	0.000
12	0.000	0.000	0.000
13	0.000	0.000	0.000
14	0.000	0.000	0.000
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16	0.000	0.000	0.000
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18	0.000	0.000	0.000
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95	0.000		

Query Match 80.3%; Score 409.4; DB 4; Length 696;
Best Local Similarity 90.5%; Pred. No. 2.6e-109;
Matches 448; Conservative 0; Mismatches 46; Indels 1

QY	15	ggaagacacgcttggcccgagcccaactatgattagagcaactgccttggtccagaccac	74
Db	15	ggaagacacacattttggcccgagcccaactatgatgagcaggccaactgccttggtccagaccac	74
QY	75	agagtggagcgctgttccaagacgctgggagtgggatggcgatctccaccgggtttacaatga	134
Db	75	agagtggagcgctgttccaagacgctgggagtgggatggcgatctccaccgggtttacaatga	134
QY	135	caacgcctctcgaggctagagaaagcagagccgctgtgcatggtcaggccttggaagc	194
Db	135	caacgcctctctcgaggctagagaaagcagagccgctgtgcatggtcaggccttggaagc	194
QY	134	caatacccttctgcagactgggaagcagagcgccctctgcatsgttcaggccctgcgaacg	193
Db	134	caatacccttctgcagactgggaagcagagcgccctctgcatsgttcaggccctgcgaacg	193
QY	195	tgacctggaagagaacattaaagaaggcgaataagtgatctcgctactcccaaatctccaa	254
Db	195	tgacctggaagagaacattaaagaaggcgaataagtgatctcgctactcccaaatctccaa	254
QY	194	tgacctggagagaaacatttaagaaggcgcaaaaagtcgacccgagacaccttaaaatcgccaa	253
Db	194	tgacctggagagaaacatttaagaaggcgcaaaaagtcgacccgagacaccttaaaatcgccaa	253
QY	255	gcctatacgaatttgagctttctgctgcaccagcatgaagacataccgagctaaattctg	314
Db	255	gcctatacgaatttgagctttctgctgcaccagcatgaagacataccgagctaaattctg	314
QY	315	tggagtatgtaccgacggccgatgctgtcacccccccagaaaccaaccctgcgcgtgga	374
Db	315	tggagtatgtaccgacggccgatgctgtcacccccccagaaaccaaccctgcgcgtgga	374
QY	314	cggggtgtgcacagacggcgctgtgcacaccgcacagaaaccacacactctgcgcgtgga	373
Db	314	cggggtgtgcacagacggcgctgtgcacaccgcacagaaaccacacactctgcgcgtgga	373
QY	375	gttcaagtgccttgacggcgaggtcatgaagaagaacatgatgttcatacagaacctgtgc	434
Db	375	gttcaagtgccttgacggcgaggtcatgaagaagaacatgatgttcatacagaacctgtgc	434
QY	435	ctgccattacaactgtcccggagacaatgacatctttgaatcgctgtactacagaagat	494
Db	435	ctgccattacaactgtcccggagacaatgacatctttgaatcgctgtactacagaagat	494
QY	495	gtacggagacatggc	509
Db	495	gtacggagacatggc	509

Db 494 GTACGGAGACATGGC 508

RESULT 8
AA373233

LOCUS	AA373233	436 bp	mRNA	EST	21-APR-1997
DEFINITION	EST85240 HSC172 cells I Homo sapiens cDNA 5' end similar to connective tissue growth factor, mRNA sequence.				

ACCESSION	CONNECTIVE TISSUE GROW
AA373233	GI-2025553
AA373233	GI-2025553

VERSION AA373233.1 GI:20233333
KEYWORDS EST.
SOURCE human.

SOURCE	ORGANISM	HUMAN.
		Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., Fitzhugh, W.M., Frichman, J.L., Geoghagen, N.S., Glodak, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanco, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Springs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.F., Ferrie, A.A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hwang, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE	96026280
COMMENT	Other_ESTs: THC166347

Contact: Kerlavage, AR
Bioinformatics

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavetigr.org
For clone availability, additional sequence and expression

information related to this EST, please check Index (<http://www.tigr.org/tdb/hg1/hg1.html>)

FEATURES	Location/Qualifiers
source	1. .436

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/note="Organ: lung Vector:

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115 2 123 2 115 2 83 4
; Site_2: XhoI"
/note="Organ: lung; vector:

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BASE COUNT	115 a	122 c	115 g	82 e
ORIGIN				

100

Query Match	78.88;	Score 402;	DB
Best Local Similarity	97.98;	Pred. No. 3.4e	

Matches 427; Conservative 0; Mismatches

Qy 1 g c g g c t t a c c g a c t g g a a g a c a c g t t t g g c c c a g a c c c

Db 2 GCGGCTTACCGACTGGAAGACACGTTGGCCCCAGACCC

Qy 61 ctggtccagaccacagagtggagcgctgttccaagac

was primed with a Not I - oligo(dT) primer [5',
TCTTACCAATCTGAAGTGGAGCCGAGTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7713 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino.
143 c 133 g 128 t 4 others

BASE COUNT	169 a	143 c	133 g	128 t	4 others
ORIGIN					

Query Match	77.38;	Score 394;	DB 159;	Length 577;
Best Local Similarity	99.38;	Pred. No. 8.3e-105;		
Matches 416; Conservative	0;	Mismatches 1;	Indels 2;	Gaps 2;

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RESULT	10	EST	21-SEP-2000
BB816120	BB816120	595 bp	EST
LOCUS	RG5-B01	140600-032-B01	BN0193 Homo sapiens
DEFINITION	RG5-B01	140600-032-B01	BN0193 Homo sapiens
ACCESSION	BB816120		
VERSION	BB816120.1	GI:10248354	
KEYWORDS	EST.		
	human.		

SOURCE ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Carnivora; Canidae; Canis lupus
1 (bases 1 to 595)

REFERENCE
Nagai, M., et al., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Dias Neto, E., da Silva, W. Jr., Zago, M. A., Bordoni, S., Coscar, F. F., D. H. Nagai, M. A., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, A. J., Brundin, G. H., Matsumura, A., Baia, G. S., Simpson, A. J., O'Hare
Brundin, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare
M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J., and
Simpson, A. J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	PROC. NATL. ACAD. SCI. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20020663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP Brazil Tel: +55-11-2704922

62	CTGTCTCCAGCACAGAGTGNAGCGCCTGTGTCCAAGACCTGTGGGATGGGCATCTCCACC	121
121	Cgggttaccaaatgaacaacgcctctcgaggctagagaagcagagccgcctgtgcgatgctc	180
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241	cccaaaatctccaagcctatcaagtttdagcttcttgctgcaccagcatgaagacatac	300
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361	accctgcggg-tggagttcaagtgccctgacggcgaggtcatgaagaagaacatgatgtt	419
362	AACCTGCCGGTTGGAGTTCAAGTGCCTGACGCGAGGTCTATGAAG-AGGACATGATGTT	420
420	catcaagaacctgtgcc	435
421	CATCAAGACCTGTGCC	436

RESULT	9	EST	10-JAN-1996
N32344		577 bp	cdna clone
LOCUS	N32344	mRNA	
DEFINITION	YX72a09.r1 Soares melanocyte 2NbHM Homo sapiens		
	IMAGE:267256 5', similar to gb:M92934 CONNECTIVE TISSUE GROWTH		
	FACTORS, HUMAN, mRNA sequence.		

ACCESSION N32344
 VERSION N32344.1 GI:1152743
 KEYWORDS EST,
 FACTOR PRECURSOR (HUMAN),, MINIMA SEQUENCE

SOURCE	ORGANISM	REFERENCE AUTHORS
human.	Homo sapiens	
Eukaryota; Euthazia;	Chordata; Vertebrata; Euteleostei	
Mammalia; Catarrhini; Primates;	Catarrhini; Hominoideae; Homo.	
1 (bases 1 to 577)		
Miller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hobbins, M., Hultman, M., Kucaba, T., Le M., Lennon, G., Marra, M., Parsons, Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Water-		
R., Williamson, A., Wohlmann, P., and Wilson, R.		

TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 1990

TEL: 314 286 1800
 FAX: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 340
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL: contact the
 IMAGE Consortium (info@image.llnl.gov) for further information
 Insert Length: 1770 Std Error: 0.00
 Seq primer: T7
 Seq primer sequence stop: 340.

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FEATURES
  source
    high quality sequence
    Location/Qualifiers
      1..577
        /organism="Homo sapiens"
        /db_xref="GDB:3876898"
        /db_xref="taxon:9606"
        /clone="IMAGE:267256"
        /clone_lib="Soares melanocyte 2NbHM"
        /sex="Male"
        /tissue_type="melanocyte"
        /lab_host="DH10B (ampicillin resistant)"
        /notes="vector: pT73D (Pharmacia) with a modified
        read number: site 1: Not I; Site 2: Eco RI; 1st stra

```

Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl1-&t2-RC5-BN0193-140
600-032-BN01&t3-2000-06-14&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 3
High quality sequence stop: 357.

FEATURES

source
1. .595
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0193"
/dev_stage="Adult"

/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 177 a 147 c 135 g 136 t

ORIGIN

Query Match 71.2%; Score 363.2; DB 140; Length 595;

Best Local Similarity 97.9%; Pred. No. 9e-96;

Matches 368; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 135 caacgctctgcaggctagagaagcagccgctgtgcattgctcagcgttcggaagc 194

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Db 3 CAACGCCCTCTGCAGGCTAGAGAAGCAGAGCGCGCTGTGCATGCTCAGGCTTCGGATGT 62

|||||

QY 195 tgacctggaagagaacaattagaaggcaaaagtgcctcgtactccccaaatctccaa 254

|||||

Db 63 TGACCTGGAAGAAACATTAAGAAGGCGAAGATGTCGCTACTCCCAAAATCTCCAA 122

|||||

QY 255 gctctacaagtcttgagctttctggtcaccagcagcagacacacacagcagcattctg 314

|||||

Db 123 GCCTATCAAGTTTGAGCTTTCTGGCTGCACCATGATGAAGCATACCGAGCTAAATCTG 182

|||||

QY 315 tgagtgatgcacgacgcccgtatgctgcaccccccacagacacaccacctgcggtgga 374

|||||

Db 183 TGGAGTATGATACCGACGCGCGCTGCTGCACCCGCCACAGAACACACACCTCGCGTGGGA 242

|||||

QY 375 gtcaagtccctgacgacgaggtcatgaagaagaacatgatgttcaagacctgtgc 434

|||||

Db 243 GTTCAAGTGCCTGCACGCGGAGGTCATGAAGAAGAACATGATGTTCAAGACCTGTGC 302

|||||

QY 435 ctgcattacaactgtcccgagacaaatgacatcttgaatcgctgtactacaggaagat 494

|||||

Db 303 CTGCCATTACAAGTGTCCCGAGACATGACATCTTTGAATCGCTGTACTACAGGACGAT 362

|||||

QY 495 gtacggagacatggca 510

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Db 363 AGACGGAGACATGGCA 378

RESULT 11

BE166172/c

LOCUS

DEFINITION

MR3-HT0489-250200-103-a05 HT0489 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BE166172

VERSION

BE166172.1 GI:8628893

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 415)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

TITLE

JOURNAL

MEDLINE

COMMENT

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl1-&t2-MR3-HT0489-250
200-103-a05&t3-2000-02-25&t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 415.

Location/Qualifiers

1. .415

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0489"

/dev_stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 76 a 109 c 126 g 104 t

ORIGIN

Query Match 68.2%; Score 348; DB 164; Length 415;

Best Local Similarity 97.3%; Pred. No. 2.3e-91;

Matches 354; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 gcggcttaccgactggaagacacgcttggccagaccccaactatgattagagccaactgc 60

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Db 366 GCGCTTACCGACTGGAAGACACGTTTGGCCACACCACTATGATTAGACCACTGC 307

|||||

QY 61 ctggtccagaccacagagtgaggcgctgttccaaagacctgtggatgggaatctccacc 120

|||||

Db 306 CTGCTCCAGACCACAGAGTGGAGCGCTGTTCAGACCTGTGGATGGCATCTCCACC 247

|||||

QY 121 cgggttaccatgacaacgctcctcagcagtagaagaagcagcccgctgtgcatgctc 180

|||||

Db 246 CGGTTTACCAATGACAACGCTCTCTGCAGGCTAGAGAAGCGCCCTGCGCATGGTC 187

|||||

QY 181 aggccttgcgaagctgacctgggaagagaacattaaaggagcgaagagtcgctact 240

|||||

Db 186 AGGCTTGGCGAGCTGACCTGGAAGACAACTTAAGAAGGCGCAAAAGTGCATCCGTACT 127

|||||

QY 241 cccaaaatctccaaagcctataaagtttgcgctttctggtgaccagcatgaagacatac 300

|||||

Db 126 CCCAAATCTCCAAGCCTATCAAGTTTTCAGCTTCTGGTGCACCAGCATGAAGACATAC 67

|||||

QY 301 cgagctaaattctgtgagtagtgtaaccgacgagccgagtgctgacccccccacagaccacc 360

|||||

Db 66 CGAGCTAAATTTCTGGAGTATGTACCGAGCGCGGATGCTGTCACCCCCACAGTCAACACG 7

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QY 361 accc 364

|||

Db 6 CACC 3

|||||

RESULT 12

BQ926068	631 bp	mRNA	EST	02-OCT-2000
MR0-BN0115-210800-006-g03 BN0115 Homo sapiens cDNA, mRNA sequence.				
BQ926068				
BQ926068	1	GI:10452144		
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed			
JOURNAL	sequence tags			
MEDLINE	proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-MR0-BN0115-210800-006-g03&t3=2000-08-21&t4=1) Seq primer: puc 18 forward High quality sequence start: 44 High quality sequence stop: 631. Location/Qualifiers 1..631 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="BN0115" /dev_stage="Adult" /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
BASE COUNT	187 a	.153 c	147 g	144 t
ORIGIN				
Query Match	68.1%	Score 347.4;	DB 142;	Length 631;
Best Local Similarity	99.4%;	Pred. No. 3.9e-91;		
Matches	359;	Conservative	1;	Gaps 1;
QY	150	gctagaagcagacgcacctgtgatcgatccaggcttcgaagtgcactggagagaa	209	
Db	43	GGTAGAAGCAGGACC-GTGTGCATGGTCAGGCCCTTGGAAGCTGACCTGGAAGA	101	
QY	210	cattagaaggcgaagtgcatccgttaccataaacatcccccaagcctcataagttga	269	
Db	102	CATTAGAAGGGCAAAAGTGCCGTTACTCCCATAATCTCCAAGCTCATCAAGTTGA	161	
QY	270	gttttgtgctcacacagatgaacatacccagctgacctaattctgtgagtagtatcca	329	
Db	162	GTCTTGTGCTGCACCAGCATGAACATACCGAGCTAAATCTGTGGAGTATGACCGA	221	
QY	330	cgcccgatgctgacccccccacagacaacacacccctgccgtgaggttaagtcgctga	389	
nB	222	CGCCGATGTCGCCCCCCCCAGAACACACACCCCTGCGGTGGAGTTCAAGTCCCTGA	281	
QY	134	acaacgctcctgcaggtcgtgagagaacagacgcgcctgctgaggtcagggccttcgaag	193	
Db	134	acaacgctcctgcaggtcgtgagagaacagacgcgcctgctgaggtcagggccttcgaag	193	

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Db 25 ACAACGCTCTCGAGGCTAGAGNAGCAGAGCGGGCTGT-CACCTGAGGCGCTAGCGAGC 83
Qy 194 ctgacctggagagaacattaaagaaggcgaagtgctacccgctaccccaaaattctcca 253
Db 84 CTGACCTGGAGGAGCAATTTGAGAAAGGCAAAAGTGCATNCGAATCTCCCAAAATCTCCA 143
Qy 254 agcctacaagtttgagctttcttgctgacccagcatgaagacataccgagctaaattct 313
Db 144 AGCCTATCAAGTTTGAAGCTTCTGCTGGCTGCACAGCATGAAGGCATACCGAGCTAAATTC 203
Qy 314 gtgagtgatgaccgagcgccgctgctgaccccccacagaaacacacccctgcctg 373
Db 204 GTGAGTATGTACGACGCGCGGATGCTGACCCCGGAGGAGGAGGAGGAGGAGGAGGAGG 263
Qy 374 agttcaagtcctcgacgagcgagtgctgacgaagaacatgatgttcatcaagacctgtg 433
Db 264 AGTTCAAGTGCCTGACGCGGAGGTCATGAAGAAGAACATGATTTTCATCAAGACCTGTG 323
Qy 434 cctgcaattacaactgtcccgagagacaatgacatcttgaatcgctgtactacaggaaga 493
Db 324 CCGTCCATTACAATGTCCCGGAGACAATGACATCTTTTGAATCGCTGTACTACAGGAAGA 383
Qy 494 tgtacggagacatggca 510
Db 384 TGTACGGAGACATGGCA 400

RESULT 14
BE479129
LOCUS BE479129 388 bp mRNA EST 28-AUG-2000
DEFINITION 163702 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE479129
VERSION BE479129.1 GI:9598662
KEYWORDS EST.
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovidae; Bos.
REFERENCE 1 (bases 1 to 388)
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt.trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTTCCAGTCCAGCAGC
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 109 a 104 c 101 g 74 t
ORIGIN
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Query Match 66.7%; Score 340; DB 136; Length 388;
Best Local Similarity 93.4%; Pred. No. 5.1e-89;
Matches 355; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 130 aatgacaacgctctctcagggctagagaagcagagccgctgtgcatggtcagcccttgc 189
Db 1 AATGACAACGCAATTCCTCAGGCTGGGAAGCAGAGCGCCTCTCATGTTGTCAGGCTTCG 60
Qy 190 gaagctgacctggaaggaacattaaaggcgaaggaagtgatccctactccccaaaatc 249
Db 61 GAAGCTGACCTGGAGGAGACATTAACAAGGCAAAAGTGCTCCCGGACCCCAAAATC 120
Qy 250 tcaagcctcatcaagtttgagcttctggtgcaccagcatgaagacatacccgagctaaa 309
Db 121 TCCAAGCCTATCAAGTTTGAGCTTCTGGCTGCACAGCATGAAGACATACCGAGCTAAA 180
Qy 310 tctgtgagatgataccgagcgccgctgctgaccccccacagaaacacacccctgcg 369
Db 181 TTCTGCGGAGTGTGCACAGAGCGGCGTGTGTCACCCCGGAGAGACACCCCTTCCC 240
Qy 370 gtgagttcaagtgccctgacgagcgagtgatgaagaacatgattcatcaagacc 429
Db 241 GTGGAGTTCAAGTGTCTGTGTTGGGAGGTGATGAAGAAGACCATGATGTTTCATCAAGACC 300
Qy 430 tgtgctgctcattacaactgtcccgagagacaatgacatcttgaatcgctgtactacagg 489
Db 301 TGTGCTGCCATTACAACCTGCCCGGAGACAATGACATCTTCGAGTCACGTACTACAGG 360
Qy 490 aagatgtacggagacatggc 509
Db 361 AAGATGTATGGAGACATGGC 380

RESULT 15
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DEFINITION 601767349F1 NC1_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3983125 5',
mRNA sequence.
ACCESSION BF162951
VERSION BF162951.1 GI:11043187
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaphs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9183 row: a column: 14
High quality sequence stop: 683.
FEATURES
Location/Qualifiers
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1..800
/organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone_lib="IMAGE:3983125"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DHI0B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
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Tue Aug 21 08:16:53 2001

Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH

BASE COUNT	187 a	219 c	233 g	161 t
ORIGIN				
Query Match	66.5%; Score 339.4; DB 145; Length 800;			
Best Local Similarity	84.0%; Pred No. 9.3e-89;			
Matches	431; Conservative	0; Mismatches	76; Indels	6; Gaps 4;
QY	1 gcggcttacgcagctggagacagctgttggccagagaccacacattatgagcccaactgc 60			
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QY	61 ctggtccagaccagagtgagcgcctgttccaaagacctgtgggatgggcatctccacc 120			
Db	293 CTGGTCCAGACACAGAGTGGAGCGCCCTGTTCTAAGACCTGTGGATGGGCATCTCCACC 352			
QY	121 cgggttaccatgacaacgcctcctgcaggctagagaagcagagagccgcctgtgcattggtc 180			
Db	353 CGAGTTACCAATGACATACCTTCTGCAGACTTGAGAAGCAGAGTCGCCCTCTGCATGGTC 412			
QY	181 aggccttcgaaagctgacctgagagagacattaaaga-gggcaaaaagtgcattccgtac 239			
Db	413 AGGCCCTGCGAAGCTGACCTGGAGGAAACATTAAAGAACGGGCAAAAAGTGCATCCGGAC 472			
QY	240 tcccaaaatctccaagccttatcaagtttgagctttctggtgcaccagcatgaagacata 299			
Db	473 ACCTAAATCGCCAGCCTGTCAAGTTTGAGCTTTCTGGCTGCAACCATGTGAGAGACCAT 532			
QY	300 cc--gagctaaattctgtgagtgatgtaccgacggccgatgtgaacccccacagaaac 357			
Db	533 ACAGGGGCTAAGTCTGCGGGGTGTCACAGACGGGCGCTGTGCACACCCGCCAGCAAGC 592			
QY	358 accacccctccggtgagttcaagtgcctgcagcggcgaggtcatg-aagaagaacatgat 416			
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QY	417 gttcataaagacctgtgcctgccattacaactgtcccggagagacaatgacatctttgaatc 476			
Db	653 GTTCATCAAGAC--TGTGCTGGCATTAACACTGTTCTCTGGGGACAATGCCCTCTTTGAGTC 710			
QY	477 gctgtactacaggaagatgtacggagacatggc 509			
Db	711 CCTGTATACAGGAAGATGTACGGGGACATGGC 743			

Search completed: August 20, 2001, 21:46:23
Job time: 1349 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2001, 22:04:44 ; Search time 61.48 Seconds
(without alignments)
167.633 Million cell updates/sec

Title: US-09-461-646-2_COPY_180_349

Perfect score: 948

Sequence: 1 AAYRLEDTGPDPTMIRAN.....PGDNDFESLYRKMYGDMA 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601:*

- 1: /SIDSL1/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL1/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL1/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL1/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL1/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSL1/gcgdata/geneseq/geneseq/AA1985.DAT:*
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- 10: /SIDSL1/gcgdata/geneseq/geneseq/AA1989.DAT:*
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- 22: /SIDSL1/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	172	21	AAV92941
2	948	100.0	347	18	AAW12694
3	948	100.0	349	16	AAW79964
4	948	100.0	349	18	AAW09089
5	948	100.0	349	19	AAW11302
6	948	100.0	349	18	AAW62084
7	948	100.0	349	20	AAW18361
8	948	100.0	349	20	AAW81425
9	948	100.0	349	21	AAV92939
10	948	100.0	349	21	AAV92940
11	948	100.0	349	21	AAV44755

ALIGNMENTS

RESULT 1

AAV92941
ID AAV92941 standard; Protein; 172 AA.

XX AC AAV92941;

XX DT 08-NOV-2000 (first entry)

XX DE Human connective tissue growth factor protein fragment.

XX KW Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;
XX KW Fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;
XX KW Hypertrophic scarring; atherosclerosis; diabetic nephropathy; retinopathy;
XX KW Hypertension; cardiovascular disorder; wound healing; bone repair.

XX OS Homo sapiens.

XX PN WO200035939-A2.

XX PD 22-JUN-2000.

XX PF 14-DEC-1999; 99WO-US29654.

XX PR 14-DEC-1998; 98US-0112240.

XX PR 14-DEC-1998; 98US-0112241.

XX PA (UYMI-) UNIV MIAMI.

XX PA (FIBR-) FIBROGEN INC.

XX PI Grotendorst GR, Neff TB;

XX DR WPI; 2000-431568/37.

XX DR N-PSDB; AAA11281.

XX

Human connective t
Human connective t
Rat connective tis
Beta-IG-M2. Mus m
Murine Fisp12. Mu
Mouse connective t
Amino acid sequenc
Bovine connective
Mouse connective t
Rat connective tis
Human cancer assoc
Bovine mammary tis
Chicken nov protei
Beta-IG-M1. Mus m
Human cysteine ric
Human monocyte mat
Human cancer assoc
Connective tissue
Human CTGF-2. Hom
Mouse putative mat
Mouse WISP-1 prote
Human WISP-3 prote
Human putative mat
Human connective t
Human WISP-3 prote
Human growth facto
Human connective t
Human WISP-1 varia
Human putative mat
Human WISP-1 varia
Human WISP-1 varia
Human WISP-1 varia
Human WISP-1 prote

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PT New fragment of connective tissue growth factor (CTGF) polypeptide
 PT having mitogenic activity, useful in wound healing, bone and tissue
 PT repair -
 XX

PS Disclosure: Fig 3; 71pp; English.

XX This sequence represents a fragment of the human connective tissue
 CC growth factor (CTGF) polypeptide which has mitogenic activity. The
 CC sequence covers the amino acids encoded by exons 4 and 5 of the full
 CC length cDNA sequence (AA112694). The protein can be used to raise
 CC antibodies which specifically bind to CTGF and are used to treat a
 CC CTGF-associated disease or disorder, e.g. a fibroproliferative
 CC disease/disorder such as kidney fibrosis, scleroderma, pulmonary
 CC fibrosis, liver fibrosis, arthritis, hypertrophic scarring,
 CC atherosclerosis, diabetic nephropathy and retinopathy, hypertension,
 CC kidney disorders, angiogenesis-related disorders, skin fibrotic
 CC disorders, and cardiovascular disorders. The protein is also useful in
 CC wound healing, bone and tissue repair.

XX Sequence 172 AA;

Query Match 100.0%; Score 948; DB 21; Length 172;
 Best Local Similarity 100.0%; Pred. NO. 4e-86;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDPPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSLCMV 60
 DB 3 aayrledtfgpdpptmiranclvqttewsacsktcgmgistrtvndnascrlckqslcmv 62
 QY 61 RPEADLEENIKGKKCIPTKISKPIKFLSGCTSMKTYRAKFCGCTDGRCTPHRTT 120
 DB 63 rpeadleenikgkckirtptkiskpikfslsgctsmktyrakfcgctdgrcctphrtt 122

QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPGDNDIFESLYYRKMVGDMA 170
 DB 123 tlpvefkcpdgevmkmmfiktacachyncpgdndifeslyyrkmygdma 172

RESULT 2

AAW12694
 ID AAW12694 standard; Protein; 347 AA.

XX AAW12694;

XX 31-MAY-1997 (first entry)

XX Connective tissue growth factor.

XX Connective tissue growth factor; CTGF; bone; cartilage; vulnary;
 KW wound healing; osteoporosis; osteoarthritis; osteochondrytis.

XX Mus sp.

XX WO9638168-A1.

XX 05-DEC-1996.

XX 31-MAY-1996; 96WO-US08210.

XX 31-MAY-1996; 96WO-US08140.

XX (GROT/) GROTEENDORST G R.

XX GROTEENDORST GR;

XX WPI; 1997-042658/04.

XX N-PSDB; AAT59618.

XX Connective tissue Growth Factor composition - for inducing bone,
 PT tissue and cartilage formation and wound healing

PS Disclosure: Fig 1C1-3; 60pp; English.

XX Connective tissue growth factor (CTGF) (AAW12694) is a cysteine-rich
 CC mitogenic protein which is selectively induced in fibroblasts after
 CC activation with transforming growth factor beta (TGF-beta).
 CC Recombinant CTGF can be produced in prokaryotic or eukaryotic host
 CC cells utilising an isolated CTGF gene (AAT59618). Compsns.
 CC comprising CTGF, pref. in combination with TGF-beta, are used to
 CC induce bonding formation, e.g. to treat osteoporosis,
 CC osteoarthritis and osteochondrytis, to induce tissue and cartilage
 CC formation, and to induce wound healing. It can also be used in
 CC culture systems e.g. to expand stem cells or chondrocytes prior to
 CC re-implantation. CTGF is more stable to protease degradation than
 CC other growth factors used as prior art wound healing agents.

XX Sequence 347 AA;

Query Match 100.0%; Score 948; DB 18; Length 347;
 Best Local Similarity 100.0%; Pred. No. 9.1e-86;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDPPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSLCMV 60
 DB 178 aayrledtfgpdpptmiranclvqttewsacsktcgmgistrtvndnascrlckqslcmv 237

QY 61 RPEADLEENIKGKKCIPTKISKPIKFLSGCTSMKTYRAKFCGCTDGRCTPHRTT 120
 DB 238 rpeadleenikgkckirtptkiskpikfslsgctsmktyrakfcgctdgrcctphrtt 297

QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPGDNDIFESLYYRKMVGDMA 170
 DB 298 tlpvefkcpdgevmkmmfiktacachyncpgdndifeslyyrkmygdma 347

RESULT 3

AAW79964
 ID AAW79964 standard; Protein; 349 AA.

XX AAW79964;

XX 12-JUN-1996 (first entry)

XX Connective tissue growth factor.

XX Connective tissue growth factor; CTGF; wound healing; vulnary;
 KW cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis
 KW therapy; mitogen.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 28 /label= N-glycosylation_site

FT Modified-site 225 /label= N-glycosylation_site

FT US5408040-A.

XX 18-APR-1995.

XX 30-AUG-1991; 91US-0752427.

XX 30-AUG-1991; 91US-0752427.

XX 14-DEC-1993; 93US-0167628.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Bradham DM, Grotendorst GR;

XX WPI; 1995-161147/21.

XX N-PSDB; AAT04226.

XX New connective tissue growth factor - used to develop prods. for
 PT

PT wound healing and for diagnosis and therapy of cell proliferative disorders.
 XX
 PS
 XX
 XX
 CC Claim 1; Column 19-20; 12pp; English.
 CC Novel human connective tissue growth factor (CTGF) (AAR79964) is related immunologically and biologically to platelet-derived growth factor (PDGF), but is the product of a distinct gene. CTGF is mitogenic and also a chemotactic agent for cells. It is produced by endothelial and fibroblastic cells, and probably acts as a growth factor in wound healing. Recombinant CTGF can be obtained by expression of cDNA clone DB60R32 (AAT04226) in transformed host cells. It is used to accelerate wound healing, and to raise antibodies useful in detecting disorders associated with overgrowth of cells, such as cancer, fibrotic diseases and atherosclerosis.
 XX
 SQ Sequence 349 AA;
 Query Match 100.0%; Score 948; DB 16; Length 349;
 Best Local Similarity 100.0%; Pred. No. 9.2e-86;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAYRLETFGDPPTMIRANCLVQTTEWSACSKTCGMISTRVTNDNASCRLEKQSRCLMV 60
 DB 180 aayrledtfgdpptmirancvlqttewsacsktcgmistrvtndnascrleqsrclmv 239
 QY 61 RPEADLEENIKGKICIRTPKISKPIKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 120
 DB 240 rpeadleenikgkicirtpkiskpikfelsgctsmktyrakfcgvtgrrcctphrtt 299
 QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 170
 DB 300 tlpvefkcpdgevmkmmfiktachyncpgdndifeslyyrkmygdma 349
 RESULT 4
 AAW09089
 ID AAW09089 standard; Protein; 349 AA.
 AC AAW09089;
 XX
 XX 26-APR-1997 (first entry)
 DT Human connective tissue growth factor.
 DE
 DE Human connective tissue growth factor.
 KW Connective tissue growth factor; CTGF; mitogen; cell proliferation; wound healing; cancer; tumour; fibrosis; glaucoma; atherosclerosis; scleroderma; arthritis; liver cirrhosis; scar; diagnosis; therapy.
 KW
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 28
 FT /label= glycosylation
 FT /note= "potential N-glycosylation site"
 FT Modified-site 225
 FT /label= Glycosylation
 FT /note= "potential N-glycosylation site"
 XX
 PN W09638172-A1.
 XX
 XX 05-DEC-1996.
 XX
 XX 31-MAY-1996; 96WO-US08140.
 XX
 XX 31-MAY-1996; 96WO-US08140.
 PR
 XX (UYSF-) UNIV SOUTH FLORIDA.
 PA
 XX Bradham DM, Grotendorst GR;
 PI
 XX WPI; 1997-042659/04.
 DR

DR N-PSDB; AAT45360;
 XX N-PSDB; AAT58534.
 XX
 PT Connective tissue growth factor coding sequence and protein - used in the treatment of proliferative disorders and to accelerate wound healing
 PT
 PS
 XX Claim 19; Page 50-52; 76pp; English.
 XX
 CC Novel human connective tissue growth factor (CTGF) (AAW09089) is a PDGF-immunorelated protein that may play a significant role in the normal development, growth and repair of human tissue and probably functions as a growth factor in wound healing. CTGF may be involved in diseases in which there is an overgrowth of connective tissue cells, such as cancer, tumour formation and growth, fibrotic diseases (e.g. pulmonary fibrosis, kidney fibrosis, glaucoma) and atherosclerosis. Recombinant CTGF can be produced in transformed host cells utilising a cDNA clone isolated from a HUVEC library. It can be used to accelerate wound healing. CTGF inhibitors can be used to treat atherosclerosis and fibrotic diseases such as scleroderma, arthritis, liver cirrhosis, and scarring.
 XX
 SQ Sequence 349 AA;
 Query Match 100.0%; Score 948; DB 18; Length 349;
 Best Local Similarity 100.0%; Pred. No. 9.2e-86;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAYRLETFGDPPTMIRANCLVQTTEWSACSKTCGMISTRVTNDNASCRLEKQSRCLMV 60
 DB 180 aayrledtfgdpptmirancvlqttewsacsktcgmistrvtndnascrleqsrclmv 239
 QY 61 RPEADLEENIKGKICIRTPKISKPIKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 120
 DB 240 rpeadleenikgkicirtpkiskpikfelsgctsmktyrakfcgvtgrrcctphrtt 299
 QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 170
 DB 300 tlpvefkcpdgevmkmmfiktachyncpgdndifeslyyrkmygdma 349
 RESULT 5
 AAW11302
 ID AAW11302 standard; Protein; 349 AA.
 XX
 AC AAW11302;
 XX
 XX 18-MAR-1997 (first entry)
 DT Connective tissue growth factor.
 DE
 DE Connective tissue growth factor.
 KW Connective tissue growth factor; CTGF; human; connective tissue cell; proliferative disease; platelet-derived growth factor; PDGF; development; tissue growth; repair; umbilical vein endothelial cell; HUVE cell; antibody; wound healing; cancer; fibrotic disease; atherosclerosis; inhibitor; protease degradation; growth factor; therapy.
 KW
 XX Homo sapiens.
 OS
 XX
 PN US585270-A.
 XX
 XX 17-DEC-1996.
 PD
 XX 30-AUG-1991; 91US-0752427.
 PF
 XX 30-AUG-1991; 91US-0752427.
 PR
 PR 14-DEC-1993; 93US-0167628.
 PR 10-FEB-1995; 95US-0386680.
 XX
 XX (UYSF-) UNIV SOUTH FLORIDA.
 PA
 XX Bradham DM, Grotendorst GR;
 PI

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XX WPI; 1997-051180/05.
XX DR N-PSDB; AAT51234.
XX
XX New nucleic acid encoding connective tissue growth factor - useful
XX PT for accelerating wound healing, also for diagnosis and treatment of
XX PT proliferative disease
XX
XX Claim 9; Column 15-18; l1pp; English.
XX
XX This sequence represents the human connective tissue growth factor
XX (CTGF). CTGF is related immunologically and biologically to
XX platelet-derived growth factor (PDGF), but is encoded by an unrelated
XX gene. CTGF is thought to play a significant role in the normal
XX development, growth, and repair of human tissue, similarly to PDGF. The
XX cDNA encoding this sequence was isolated by screening a cDNA library from
XX human umbilical vein endothelial (HUVE) cells with anti-PDGF antibodies.
XX CTGF can be used to accelerate wound healing. Also, elevated levels of
XX CTGF may be diagnostic of proliferative diseases involving outgrowth of
XX connective tissue cells, such as cancer, fibrotic disease and
XX atherosclerosis. All of these diseases can be treated with reagents
XX reactive with CTGF, such as antibodies (which can also serve as assay
XX reagents). Antisense nucleic acids, and ribozymes could also be used to
XX inhibit CTGF production. The advantage with using CTGF is that it is
XX more stable, and less susceptible to protease degradation than PDGF, and
XX other growth factors involved in wound healing. This is believed to be
XX due to the high Cys content.
XX
XX Sequence 349 AA:
SQ
Query Match 100.0%; Score 948; DB 18; Length 349;
Best Local Similarity 100.0%; Pred. No. 9.2e-86;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAYLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60
Db 180 aayrledtfgpdtmirancvlqttewsacsctcmgistrvndnascrlkqslcmv 239
QY 61 RCEADLEENIKGKCIPTPKISKPIKELSGCTSMKTYRAKFCGCTDGRCCTPHRTT 120
Db 240 rpceadleenikgkciptpkiskpikfsgctsmktyrakfcgctdgrcctphttt 299
QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
Db 300 tlpvefkcpdgevmkmmfiktachyncpgdndifeslyyrkmygdma 349
RESULT 6
AAW62084
ID AAW62084 standard; Protein; 349 AA.
XX
XX AC AAW62084;
XX
XX DT 15-SEP-1998 (first entry)
XX
XX Human connective tissue growth factor.
XX
XX Human; connective tissue growth factor; CTGF; PDGF; diagnosis; cancer;
XX platelet derived growth factor; ameliorating cell proliferative disorder;
XX atherosclerosis; fibrotic disease.
XX
XX Homo sapiens.
XX
XX US5783187-A.
XX
XX 21-JUL-1998.
XX
XX 11-SEP-1996; 96US-0712302.
XX
XX 30-AUG-1991; 91US-0752427.
XX
XX 14-DEC-1993; 93US-0167628.
XX
XX 11-SEP-1996; 96US-0712302.

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XX (UYSF-) UNIV SOUTH FLORIDA.
XX PA Bradham DM, Grotendorst GR;
XX PI
XX WPI; 1998-426958/36.
XX DR N-PSDB; AAV38085.
XX
XX Ameliorating cell proliferative disorder associated with connective
XX tissue growth factor - comprises the administration of an antibody
XX which binds to connective tissue growth factor and not to
XX platelet-derived growth factor
XX
XX Example 6; Column 17-20; l1pp; English.
XX
XX A method has been developed for ameliorating a cell proliferative
XX disorder associated with connective tissue growth factor (CTGF). The
XX method comprises the administration of an antibody or its fragment that
XX binds to CTGF and not to platelet-derived growth factor (PDGF), to the
XX site of the disorder. CTGF is related immunologically and biologically
XX to PDGF. The present sequence represents CTGF. The method is used to
XX treat conditions involving the overgrowth of connective tissue cells
XX such as cancer, atherosclerosis and other fibrotic diseases.
XX
XX Sequence 349 AA:
SQ
Query Match 100.0%; Score 948; DB 19; Length 349;
Best Local Similarity 100.0%; Pred. No. 9.2e-86;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAYLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60
Db 180 aayrledtfgpdtmirancvlqttewsacsctcmgistrvndnascrlkqslcmv 239
QY 61 RCEADLEENIKGKCIPTPKISKPIKELSGCTSMKTYRAKFCGCTDGRCCTPHRTT 120
Db 240 rpceadleenikgkciptpkiskpikfsgctsmktyrakfcgctdgrcctphttt 299
QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
Db 300 tlpvefkcpdgevmkmmfiktachyncpgdndifeslyyrkmygdma 349
RESULT 7
AAW18361
ID AAW18361 standard; Protein; 349 AA.
XX
XX AC AAW18361;
XX
XX DT 20-AUG-1999 (first entry)
XX
XX Human connective tissue growth factor.
XX
XX CTGF; connective tissue growth factor; human; fibrotic disease;
XX cell proliferative disorder; atherosclerosis; diagnosis.
XX
XX Homo sapiens.
XX
XX US5916756-A.
XX
XX 29-JUN-1999.
XX
XX 20-JUN-1997; 97US-0880031.
XX
XX 14-DEC-1993; 93US-0167628.
XX
XX 10-FEB-1995; 95US-0386680.
XX
XX 11-SEP-1996; 96US-0712302.
XX
XX 20-JUN-1997; 97US-0880031.
XX
XX (UYSF-) UNIV SOUTH FLORIDA.
XX PA Bradham DM, Grotendorst GR;
XX PI

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PI  Grotendorst GR;
XX  WPI: 2000-431565/37.
DR  N-PSDB; AA11278.
XX
XX  Fragment of connective tissue growth factor, useful for treating
XX  fibroproliferative diseases or disorders, including kidney fibrosis,
XX  scleroderma, arthritis, hypertrophic scarring, atherosclerosis, diabetic
XX  nephropathy and retinopathy
XX
XX  Claim 2, 3; Fig 3A-B; 74pp; English.
XX
XX  This sequence represents a human connective tissue growth factor (CTGF)
XX  polypeptide having the ability to induce extracellular matrix synthesis,
XX  collagen synthesis and/or myofibroblast differentiation. The invention
XX  relates to fragments of CTGF, especially those encoded by exons 2 and/or
XX  3, which contain the inductive activity. The protein and/or fragments
XX  can be used to raise antibodies and the coding sequence can be used to
XX  generate antisense oligonucleotides. The antibody or antisense sequence
XX  against the CTGF sequence can be used in a method to treat a
XX  CTGF-associated disease or disorder such as a fibroproliferative disease
XX  or disorder, especially selected from kidney fibrosis, scleroderma,
XX  pulmonary fibrosis, liver fibrosis, arthritis, hypertrophic scarring,
XX  atherosclerosis, diabetic nephropathy and retinopathy, hypertension,
XX  kidney disorders, angiogenesis-related disorders, skin fibrotic
XX  disorders, and cardiovascular disorders. The disease or disorder can
XX  also be selected from acute or repetitive traumas (including surgery or
XX  radiation therapy, and fibrosis of organs), diseases caused by vascular
XX  endothelial cell proliferation or migration (including cancers),
XX  inflammatory bowel disease, Crohn's disease, joint inflammation,
XX  interstitial disease, dermatological diseases, diabetes, and keloids.
XX
XX  Sequence 349 AA;
SQ

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PF  14-DEC-1999; 99WO-US29654.
XX
XX  14-DEC-1998; 98US-0112240.
PR  14-DEC-1998; 98US-0112241.
XX
XX  (UWMI-) UNIV MIAMI.
PA  (FIBR-) FIBROGEN INC.
XX
XX  Grotendorst GR, Neff TB;
XX
XX  WPI: 2000-431568/37.
DR  N-PSDB; AA11280.
XX
XX  New fragment of connective tissue growth factor (CTGF) polypeptide
XX  having mitogenic activity, useful in wound healing, bone and tissue
XX  repair -
XX
XX  Claim 2, 3; Fig 2A-B; 71pp; English.
XX
XX  This sequence represents a human connective tissue growth factor (CTGF)
XX  polypeptide which has mitogenic activity. The protein can be used to
XX  raise antibodies which specifically bind to CTGF and are used to treat
XX  a CTGF-associated disease or disorder, e.g. a fibroproliferative
XX  disease/disorder such as kidney fibrosis, scleroderma, pulmonary
XX  fibrosis, liver fibrosis, arthritis, hypertrophic scarring,
XX  atherosclerosis, diabetic nephropathy and retinopathy, hypertension,
XX  kidney disorders, angiogenesis-related disorders, skin fibrotic
XX  disorders, and cardiovascular disorders. The protein is also useful
XX  in wound healing, bone and tissue repair.
XX
XX  Sequence 349 AA;
SQ

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Query Match 100.0%; Score 948; DB 21; Length 349;
Best Local Similarity 100.0%; Pred. No. 9.2e-86;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSLRCMV 60
DB 180 aayrledfgpdptmirancvlvqttewsacsctcgmgistrvndnasrlekqslrcmv 239
QY 61 RPEADLEENIKKGCIRTPKISKPIKPELSCGTSMTKYRAKFCGVCCTDGRCCTPHRTT 120
DB 240 rpeadleenikkgcirtpkiskpikfelsgctsmktyrakfcgvcctdgrccctphrtt 299
QY 121 TLPVFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGDMA 170
DB 300 tlpvfkcpdgevmknnmmfiktachyncpgdndifeslyyrykmygdma 349

RESULT 11
AAY44755
ID AAY44755 standard; protein: 349 AA.
XX
XX AC AAY44755;
XX
XX DT 04-MAY-2000 (first entry)
XX
XX DE Human connective tissue growth factor.
XX
XX KW Connective tissue growth factor; CCN growth regulator; angiogenesis;
XX KW antiangiogenic; basic fibroblast growth factor; bFGF; neovascular;
XX KW endothelial cell proliferation; retinal; haemangioma; leukaemia;
XX KW metastasis; psoriasis; tumour; glaucoma; diabetic retinopathy; arthritis;
XX KW endometriosis; Insulin-like growth factor-binding domain; IGF;
XX KW von Willebrand factor type C repeat; Thrombospondin type 1 domain;
XX KW C-terminal cysteine knot profile; CTCK-2; human.
XX
XX OS Homo sapiens.
XX
XX PN WO200005356-A1.
XX
XX PD 03-FEB-2000.

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RESULT 10
AAY92940
ID AAY92940 standard; Protein: 349 AA.
XX
XX AC AAY92940;
XX
XX DT 08-NOV-2000 (first entry)
XX
XX DE Human connective tissue growth factor protein.
XX
XX KW Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;
XX KW fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;
XX KW hypertrophic scarring; atherosclerosis; diabetic nephropathy; retinopathy;
XX KW hypertension; cardiovascular disorder; wound healing; bone repair.
XX
XX OS Homo sapiens.
XX
XX PN WO200035939-A2.
XX
XX PD 22-JUN-2000.
XX

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XX PF 12-JUN-1998; 98US-0097179.
 XX PR 14-DEC-1993; 93US-0167628.
 XX PR 10-FEB-1995; 95US-0386680.
 XX PR 11-SEP-1996; 96US-0712302.
 XX PR 30-AUG-1991; 91US-0752427.
 XX PA (UYSF-) UNIV SOUTH FLORIDA.
 XX PI Bradham DM, Grotendorst GR;
 XX PI WPI; 2001-079389/09.
 XX DR N-PSDB; AAC87517.
 XX DR Accelerating wound healing or stimulating growth of connective tissue
 XX PT cells involves contacting the site of a wound or cells with a
 XX PT composition comprising purified connective tissue growth factor and
 XX PT transforming growth factor beta -
 XX PS Claim 1; Column 17-20; l1pp; English.
 XX CC The invention relates to methods of accelerating wound healing in a
 XX CC patient. One method involves contacting the site of the wound with a
 XX CC composition comprising purified connective tissue growth factor
 XX CC (CTGF; AAB48831) and transforming growth factor beta (TGF-beta), which
 XX CC stimulates the production of CTGF in vivo. Another method involves
 XX CC stimulating the growth of connective tissue cells by contacting the
 XX CC cells with CTGF or an active fragment thereof. CTGF is produced by
 XX CC endothelial and fibroblastic cells, both of which are present at the
 XX CC site of a wound, and is mitogenic and chemotactic for connective tissue
 XX CC cells. It has biologically similar activity to PDGF (platelet-derived
 XX CC growth factor), and is also immunologically related to it, but it is
 XX CC the product of a distinct gene. CTGF is useful for accelerating wound
 XX CC healing by stimulating the growth of connective tissue cells. CTGF, or
 XX CC its functional fragments, is more stable and less susceptible to be
 XX CC protease degradation than PDGF and other growth factors known to be
 XX CC involved in wound healing. The present sequence represents human CTGF.
 XX SQ Sequence 349 AA;
 Query Match 100.0%; Score 948; DB 22; Length 349;
 Best Local Similarity 100.0%; Pred. No. 9, 2e-86;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAYRLEDFGDPDMIRANCLVQTTWSACSKTCGMGISTRTVNDNASCRLEKQSLRCMV 60
 DB 180 aayrledtfgdpdmiranclvqtwsacsktcgmgistrtvndnasrlekqslrcmv 239
 QY 61 RPCEADLEENIKGKKCIKIRTPKISKPIKFKELSGCTSMKTYRAKFCGCTDGRCTPHRTT 120
 DB 240 rpceadleenikgkckirtpkiskpikfslsgctsmktyrakfcgctdgrctphrtt 299
 QY 121 TLPVEFKCPDGEVMMKNNMFMFKTCACHYNCPCGNDIFESLYYRMYGDMA 170
 DB 300 tlpvefkcpdgevmknnmmfiktacachyncpcgndifeslyyrkmygdma 349
 RESULT 14
 AAY24379
 ID AAY24379 standard; Protein; 347 AA.
 XX AC AAY24379;
 XX DT 17-SEP-1999 (first entry)
 XX DE Rat connective tissue growth factor.
 XX KW Human; monoclonal antibody; connective tissue growth factor; CTGF;
 KW cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
 KW skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
 KW rheumatic vascular inflammation.

XX OS Rattus sp.
 XX PN WO9933878-A1.
 XX PD 08-JUL-1999.
 XX PF 16-DEC-1998; 98WO-JP05697.
 XX PR 15-DEC-1998; 98JP-0356183.
 XX PR 25-DEC-1997; 97JP-0367699.
 XX PA (NIBS) JAPAN TOBACCO INC.
 XX PI Sakamoto S, Takigawa M, Tamatani T, Tezuka K;
 XX PI WPI; 1999-430232/36.
 XX DR N-PSDB; AAX90030.
 XX DR New monoclonal antibody reactive with connective tissue growth
 XX PT factor useful in the treatment of cell proliferation disorders
 XX PS Claim 60; Page 167-169; 212pp; Japanese.
 XX CC AAX90020 to AAX90029 encode monoclonal antibodies which react with human
 XX CC connective tissue growth factor (CTGF). AAY24369 to AAY24378 represent
 XX CC these monoclonal antibodies. The antibodies are useful in the diagnosis,
 XX CC prevention and treatment of cell proliferation disorders in which CTGF
 XX CC is implicated, including fibrosis of lung, kidney, liver and other
 XX CC tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid
 XX CC arthritis; rheumatic vascular inflammation; hepatitis; and cancer.
 XX CC The present sequence represents rat CTGF.
 XX SQ Sequence 347 AA;
 Query Match 97.7%; Score 926; DB 20; Length 347;
 Best Local Similarity 95.9%; Pred. No. 1.4e-83;
 Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAYRLEDFGDPDMIRANCLVQTTWSACSKTCGMGISTRTVNDNASCRLEKQSLRCMV 60
 DB 178 aayrledtfgdpdmiranclvqtwsacsktcgmgistrtvndntfcrlekqslrcmv 237
 QY 61 RPCEADLEENIKGKKCIKIRTPKISKPIKFKELSGCTSMKTYRAKFCGCTDGRCTPHRTT 120
 DB 238 rpceadleenikgkckirtpkiskpikfslsgctsmktyrakfcgctdgrctphrtt 297
 QY 121 TLPVEFKCPDGEVMMKNNMFMFKTCACHYNCPCGNDIFESLYYRMYGDMA 170
 DB 298 tlpvefkcpdgevmknnmmfiktacachyncpcgndndifeslyyrkmygdma 347
 RESULT 15
 AAR25566
 ID AAR25566 standard; Protein; 348 AA.
 XX AC AAR25566;
 XX DT 18-JAN-1993 (first entry)
 XX DE Beta-IG-M2.
 XX KW Transforming growth factor beta; induced; CEF-10; v-src; chicken;
 KW embryo; fibroblasts; TGF-beta.
 XX OS Mus musculus.
 XX PN EP495674-A.
 XX PD 22-JUL-1992.
 XX PF 17-JAN-1992; 92EP-0300429.

XX 18-JAN-1991; 91US-0642991.
PR 10-JAN-1992; 92US-0816270.
XX
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX PI Brunner AM, Chinn J, Neubauer MG, Purchio AF;
XX
XX DR WPI; 1992-243508/30.
XX DR N-PSDB; AAQ26422.
XX
XX PT TGF-beta induced gene family - encodes proteins involved in
XX PT growth and differentiation effects of TGF-beta-1
XX
XX PS Claim 3; Fig 2; 35pp; English.
XX
XX CC The protein sequence was deduced from the DNA sequence obtd. by
XX CC screening a cDNA library made from AKR-2B mouse cells induced with
XX CC TGF-beta1 and cyclohexamide with two probes from untreated AKR-2B
XX CC mRNA and AKR-2B mRNA from cells treated with cyclohexamide and TGF-
XX CC beta1. The proteins encoded by hybridising colonies (beta-IG-M1 and
XX CC beta-IG-M2) contain 38 Cys residues and are induced by TGF-beta1.
XX CC Beta-IG-M2 displays 50 percent homology to the CEF-10 protein
XX CC induced by v-src in chicken embryo fibroblasts. Residues 52-59
XX CC of beta-IG-M2 conform to the GCGCCXXC motif reported in the
XX CC amino half of insulin-like growth factor (IGF) binding proteins.
XX CC The C-terminal Cys rich region of beta-IG-M1, -M2 and CEF-10 contain
XX CC an amino acid sequence with strong homology to a motif found near the
XX CC C-terminal of the malarial circumsporozoite (CS) protein, which is
XX CC highly conserved among all species of malarial parasites sequenced
XX CC to date (designated region II). This motif is also found in
XX CC other proteins which have cell adhesive properties that mediate
XX CC cell-cell and cell-extracellular matrix interactions, such as
XX CC perlecan, thrombospondin, and TRAP. The proteins encoded by
XX CC TGF-beta induced genes are likely to be involved in mediation of
XX CC the biological effects of TGF-beta relating to cell growth and
XX CC differentiation. See also AAR25565.
XX
SQ Sequence 348 AA;

Query Match 97.7%; Score 926; DB 13; Length 348;
Best Local Similarity 95.9%; Pred. No. 1.4e-83;
Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
179 aayrledtfgdpdmirancvlqtewsacsktcgmgistrtvndntfcrlekgsrlcmv 238

QY 61 RPSADLEENIKGKGIKIRTPKISKPIKFSLGCTSMKTYRAKFCGVCTDGRCCCTPHRTT 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
239 rpceadleenikgkckirtpkiakpvkfslgctsvktyrakfcgvtcdgrccctphrtt 298

QY 121 TLPVFVKCPDGEVMMKMMFIKTCACHYNCPGDNDIFESLYRMYGDMA 170
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
299 tlpvfekcpdgeimkmmfiktachyncpgdndifeslyyrkmygdma 348

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2001, 22:06:59 ; Search time 72.24 Seconds
(without alignments)
48.455 Million cell updates/sec

Title: US-09-461-646-2_COPY_180_349

Perfect score: 948

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	948	100.0	348	1	US-08-468-847B-14
2	948	100.0	349	1	US-08-167-628-2
3	948	100.0	349	1	US-08-386-680-2
4	948	100.0	349	1	US-08-459-717-2
5	948	100.0	349	1	US-08-712-302-2
6	948	100.0	349	2	US-08-880-031-2
7	948	100.0	349	3	US-09-054-368-2
8	948	100.0	349	4	US-09-097-179-2
9	948	100.0	349	4	US-09-054-274-2
10	948	100.0	349	4	US-09-080-715-2
11	948	100.0	349	4	US-09-056-704-2
12	948	100.0	349	5	PCT-US96-08140-2
13	926	97.7	348	1	US-08-468-847B-15
14	540.5	57.0	351	1	US-08-468-847B-16
15	515	54.3	357	1	US-08-468-847B-17
16	487.5	51.4	379	1	US-08-468-847B-11
17	479.5	50.6	375	1	US-08-468-847B-13
18	469.5	49.5	374	1	US-08-468-847B-12
19	468.5	49.4	375	2	US-08-459-101A-2
20	141	14.9	24	2	US-08-908-526-20
21	101.5	10.7	807	1	US-07-862-021B-10
22	101.5	10.7	807	1	US-08-313-288B-10
23	101.5	10.7	807	5	PCT-US93-03164-10
24	99	10.4	18	2	US-08-908-526-15
25	96	10.1	464	3	US-08-957-063-6
26	96	10.1	664	3	US-08-957-063-18
27	95	10.0	423	2	US-08-760-797A-1

Sequence 1, Appli
Sequence 3, Appli
Sequence 16, Appl
Sequence 183, App
Sequence 13, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 8, Appli
Sequence 34, Appl
Sequence 34, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-08-468-847B-14
: Sequence 14, Application US/08468847B
: Patent No. 5780263
: GENERAL INFORMATION:
: APPLICANT: Hastings, Gregg A. and Adams, Mark D.
: TITLE OF INVENTION: Human CCN-Like Growth Factor
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
: ADDRESSEE: CECCHI, STEWART & OLSTEIN
: STREET: 6 BECKER FARM ROAD
: CITY: ROSELAND
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 INCH DISKETTE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WORD PERFECT 5.1
: CURRENT APPLICATION NUMBER: US/08/468,847B
: FILING DATE: 6 June 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: MULLINS, J.G.
: REGISTRATION NUMBER: 33,073
: REFERENCE/DOCKET NUMBER: 325800-442
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 348 AMINO ACIDS
: TYPE: AMINO ACID
: STRANDEDNESS:
: TOPOLOGY: LINEAR
: MOLECULE TYPE: PROTEIN
: US-08-468-847B-14

Query Match 100.0%; Score 948; DB 1; Length 348;
Best Local Similarity 100.0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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db	239	RPEADLEENIKKGGKCIPTPKISPKIPKELGGCTSMKTYRAKFCGVCTDGRCTPHRTT	298
QY	121	TLPVEFKCPDGEVKKNNMFIKTCACHYNCPGDNDIFESLYRKMVGDMA	170
db	299	TLPVEFKCPDGEVKKNNMFIKTCACHYNCPGDNDIFESLYRKMVGDMA	348

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	Matches 170;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps	
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QY	61	RCEADLEENIKKKKCIKTPKISKPIKFLSGGCTSMKTYRAKFCGCTDGRCTPHRTT	120			
DB	240	RCEADLEENIKKKKCIKTPKISKPIKFLSGGCTSMKTYRAKFCGCTDGRCTPHRTT	299			
QY	121	TLPEVKCPDGEVKKNNMFIKTCACHYNCPGDNDIFESLYRMYGDMA	170			
DB	300	TLPEVKCPDGEVKKNNMFIKTCACHYNCPGDNDIFESLYRMYGDMA	349			

RESULT 3
US-08-386-680-2 Application US/08386680
; Sequence 2, Patent No. 5585270
; GENERAL INFORMATION:
; APPLICANT: Grotenndorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,680
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION NUMBER: US/08/167,628
; FILING DATE: 07/07/92
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-386-680-2

Query Match	100.0%;	Score	948;	DB 1;	Length	349;
Best Local Similarity	100.0%;	Pred. No.	4.3e-83;			
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						Gaps
						0;
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Db	180	AAAYRLDTFGDPDMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRLCMV	239			
QY	61	RPCEADLEENIKGKKCIKTPKISKPIKFELSGCTSMKTYRAKFCGCTDGRCCTPHRTT	120			
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RESULT 4
US 08-459-717-2
; Sequence 2, Application US/08459717
; Patent No. 5770209
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

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D8	180	AAYRLEDTGPDPTMIRANCLVOTTENSACSKTGMGISTRVTNDNASCRLEKQSRLCMW	239		
QY	61	RPCAEADLEENIKGGKKCI RTP KISPKIFELSGCSTSMKT YRAFCGVCTDGRCCPHRTT	120		
D8	240	RPCAEADLEENIKGGKKCI RTP KISPKIFELSGCSTSMKT YRAFCGVCTDGRCCPHRTT	299		
QY	121	TLPVFECPPDGVEYNKNMF I KTCA CHYNC PGDNDFESLYYRMKGDMA	170		
D8	300	TLPVFECPPDGVEYNKNMF I KTCA CHYNC PGDNDFESLYYRMKGDMA	349		

RESULT 9
US-09-054-274-2
; Sequence 2, Application US/09054274
; Patent No. 6150101
; GENERAL INFORMATION:
; APPLICANT: University of South Florida

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; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham, Jr., Douglas M.
; TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION
; TITLE OF INVENTION: THAT ALTERS CONNECTIVE TISSUE GROWTH
; TITLE OF INVENTION: FACTOR EXPRESSION (Amended)
; FILE REFERENCE: 07414/003004
; CURRENT APPLICATION NUMBER: US/09/054,274
; CURRENT FILING DATE: 1998-04-02
; EARLIER APPLICATION NUMBER: 08/386,680
; EARLIER FILING DATE: 1995-02-10
; EARLIER APPLICATION NUMBER: 08/459,717
; EARLIER FILING DATE: 1995-06-02
; EARLIER APPLICATION NUMBER: 08/167,628
; EARLIER FILING DATE: 1993-12-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-054-274-2

Query Match      100.0%; Score 948; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60
Db 180 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 239
QY 61 RPCEADLEENIKKGKCIKIRTPKISKPIKFLSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
Db 240 RPCEADLEENIKKGKCIKIRTPKISKPIKFLSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 299
QY 121 TLPVEFKCPDGEVKNMFMFKTCACHYNCPCGNDIFESLYYRKMVGMDMA 170
Db 300 TLPVEFKCPDGEVKNMFMFKTCACHYNCPCGNDIFESLYYRKMVGMDMA 349

RESULT 10
US-09-080-715-2
; Sequence 2, Application US/09080715
; Patent No. 6190884
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John W.
; REGISTRATION NUMBER: 31,678
```

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; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-080-715-2
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Query Match      100.0%; Score 948; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60
Db 180 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 239
QY 61 RPCEADLEENIKKGKCIKIRTPKISKPIKFLSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
Db 240 RPCEADLEENIKKGKCIKIRTPKISKPIKFLSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 299
QY 121 TLPVEFKCPDGEVKNMFMFKTCACHYNCPCGNDIFESLYYRKMVGMDMA 170
Db 300 TLPVEFKCPDGEVKNMFMFKTCACHYNCPCGNDIFESLYYRKMVGMDMA 349
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RESULT 11
US-09-056-704-2
; Sequence 2, Application US/09056704
; Patent No. 6232064
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham, Jr., Douglas M.
; TITLE OF INVENTION: METHODS OF DIAGNOSING A PATHOLOGY
; TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE
; TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
; TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)
; FILE REFERENCE: 07414/003002
; CURRENT APPLICATION NUMBER: US/09/056,704
; CURRENT FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 08/386,680
; EARLIER FILING DATE: 1995-02-10
; EARLIER APPLICATION NUMBER: 08/459,717
; EARLIER FILING DATE: 1995-06-02
; EARLIER APPLICATION NUMBER: 08/167,628
; EARLIER FILING DATE: 1993-12-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-056-704-2
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Query Match      100.0%; Score 948; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60
Db 180 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 239
QY 61 RPCEADLEENIKKGKCIKIRTPKISKPIKFLSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
Db 240 RPCEADLEENIKKGKCIKIRTPKISKPIKFLSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 299
QY 121 TLPVEFKCPDGEVKNMFMFKTCACHYNCPCGNDIFESLYYRKMVGMDMA 170
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STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,847B
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-44

```
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-468-847B-15

          97.7%   Score 926; DB 1; Length 348;
Query Match      95.9%; Pred. No. 5,4e-81;
Best Local Similarity
Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps

QY       1 AAYRLEDTFGDPDMIRANCLVQTTEWSACSKTCGMGISITRVTDNNA SCRLKQSRLCMV 60
         ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db        179 AAYRLEDTFGDPDMIRANCLVQTTEWSACSKTCGMGISITRVTDNDTFCRLKQSRLCMV 231

QY       61 RCEADLEENIKKKGLCTRPKISKPTKFELSGCSTSMKITYRAKFGCVVDGRCCCTPHRTT 120
         ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
         CTPMPTKTAIVKVEFFI SACTSVKTYRAKFGCVVDGRCCCTPHRTT 121
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QY	121	TLPVEFKCPDGEVMKKNMMF	TKTCACHYNC	CGDNDIFESLYRKMYGDMA	170
DB.	299	TLPVEFKCPDGEIMKKNMMF	IKTCACHYNC	CGDNDIFESLYRKMYGDMA	348

RESULT 14
 US-08-468-847B-16
 ; Sequence 16, Application US/08468847B-
 ; Patent No. 5780263
 ; GENERAL INFORMATION:
 ; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
 ; TITLE OF INVENTION: Human CCN-Like Growth Factor
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
 ; ATTORNEYS: CARELLA, BYRNE & OSTEIN

CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468, 847B
FILING DATE: 6 June 1995

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-442
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-468-847B-16

Query Match 57.0%; Score 540.5; DB 1; Length 351;
Best Local Similarity 59.9%; Pred. No. 3.3e-44;
Matches 94; Conservative 22; Mismatches 40; Indels 1; Gaps 1;
QY 1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRCLMV 60
Db 183 AAYRQEAATLGIVSDSSANCIEQTTEWSACSKCGMGFSTRVNRNQCEMVKQTRLCMM 242
QY 61 RPEADLEENIKKGGKCIPTPKSKPKFELSGCTSMKTYRAKFCGVCTDGRCTTPHRTT 120
Db 243 RPECNE-EPSSDKKGGKCIPTPKSKPKFELSGCTSMKTYRAKFCGVCTDGRCTTPHNTK 301
QY 121 TLPEVEKCPDGEVYKMMFMFKTCACHYNCPGDNDIF 157
Db 302 TIQVEFRCPDGEVYKMMFMFKTCACHYNCPGDNDIF 338

RESULT 15
US-08-468-847B-17
; Sequence 17, Application US/08468847B
; Patent No. 5780263
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
; TITLE OF INVENTION: Human CCN-Like Growth Factor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,847B
; FILING DATE: 6 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-442
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-468-847B-17

Query Match 54.3%; Score 515; DB 1; Length 357;
Best Local Similarity 54.4%; Pred. No. 9.2e-42;
Matches 93; Conservative 25; Mismatches 51; Indels 2; Gaps 2;
QY 1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRCLMV 60
Db 187 AAYRPEATLGLVEVSDSSVNCIEQTTEWSACSKCGMGFSTRVNRNQCEMLKQTRLCMV 246
QY 61 RPEADLEE-NIKKGGKCIPTPKSKPKFELSGCTSMKTYRAKFCGVCTDGRCTTPHRT 119
Db 247 RPECQEPQPTDKKGGKCLRTKSLKAIHLQFNKCTSLHTYKPRFCGVCTDGRCTTPHNT 306
QY 120 TLPEVEKCPDGEVYKMMFMFKTCACHYNCPGDNDIF-ESLYYRKMVYGM 169
Db 307 KTIOAEFQCPDGEVYKMMFMFKTCACHYNCPGDNDIF-ESLYYRKMVYGM 357

Search completed: August 20, 2001, 22:47:51
Job time: 2452 sec

us-09-461-646-2_copy_180_349.ra1

Tue Aug 21 08:16:54 2001

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 20, 2001, 22:43:25 ; Search time 75.11 Seconds
(without alignments)
172.409 Million cell updates/sec

Title: US-09-461-646-2_COPY_180_349
Perfect score: 948
Sequence: 1 AAYRLEDTFGDPTMIRANC.....PGDNDIFESLYRKMYGDMA 170
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	349	2 A40551	connective tissue
2	926	97.7	348	2 A40578	beta IG-M2 protein
3	540.5	57.0	351	2 S20078	NOV protein - chic
4	515	54.3	357	2 I38069	gene novH protein
5	487.5	51.4	379	2 A35669	gene CYR61 protein
6	479.5	50.6	375	2 A41428	CEF-10 protein pre
7	116	12.2	2165	2 T21371	hypothetical prote
8	107	11.3	1444	2 T18856	angiogenesis inhib
9	102.5	10.8	2098	2 T18397	protein CTRP - mal
10	101.5	10.7	807	2 A38152	F-spondin - rat
11	99	10.4	712	2 A45638	immunodominant mic
12	99	10.4	803	2 A47723	F-spondin precursor
13	97	10.2	4753	1 A47437	LDL-receptor-relat
14	96.5	10.2	654	2 T29247	hypothetical prote
15	96.5	10.2	898	2 T14764	hypothetical prote
16	92	9.7	1205	2 T18517	procollagen N-endo
17	92	9.7	1274	2 T42017	cysteine rich prot
18	91	9.6	1059	2 T22545	hypothetical prote
19	90.5	9.5	651	2 T19477	hypothetical prote
20	90.5	9.5	1042	2 A57534	mucin 5AC (clone L
21	90.5	9.5	1372	2 T25933	hypothetical prote
22	90.5	9.5	4006	2 T09070	probable tenascin
23	89.5	9.4	388	2 A39756	circumsporozoite p
24	89.5	9.4	1178	1 A39804	thrombospondin pre
25	89	9.4	2167	2 T34395	hypothetical prote
26	88.5	9.3	1025	2 S50911	metallothionein-2
27	88	9.3	1025	2 T42626	secreted leucine-r
28	88	9.3	2910	2 T42214	otogelin - mouse
29	87.5	9.2	412	1 OZ2QAF	circumsporozoite p

30 87.5 9.2 424 2 A54533 circumsporozoite p
31 87.5 9.2 442 2 A54529 circumsporozoite p
32 87.5 9.2 957 2 T15976 hypothetical prote
33 87 9.2 152 2 I47109 high-sulfur wool m
34 87 9.2 732 2 S47073 finger protein HZF
35 87 9.2 837 2 A42112 mucin-like peptide
36 87 9.2 1170 1 TSHUP1 thrombospondin 1 p
37 86 9.1 388 2 C6164 circumsporozoite p
38 86 9.1 951 2 T00260 hypothetical prote
39 86 9.1 1170 2 A40558 thrombospondin 1 p
40 85.5 9.0 724 2 A48569 antigen Em100 - Ei
41 85 9.0 111 2 T34565 hypothetical prote
42 85 9.0 152 1 KRSHHC keratin high-sulfu
43 85 9.0 152 2 I47112 high-sulfur wool m
44 85 9.0 182 2 I47105 high-sulfur wool m
45 85 9.0 1101 2 T16840 hypothetical prote

ALIGNMENTS

RESULT 1
A40551
connective tissue growth factor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: A40551; S44205
R:Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A:Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human v
A:Reference number: A40551; MUID:91373462
A:Accession: A40551
A:Molecule type: mRNA
A:Residues: 1-349 <BRA>
A:Cross-references: GB:M92934; GB:M36965; GB:S56201; NID:g180923; PIDN:AA91279.1; PI
R:Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
submitted to the EMBL Data Library, April 1994
A:Description: Differential cloning and expression of human connective tissue growth
A:Reference number: S44205
A:Accession: S44205
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-349 <OEM>
A:Cross-references: EMBL:X78947; NID:g474933; PID:g474934

Query Match 100.0%; Score 948; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAYRLEDTFGDPTMIRANCLVOTTEWSACSKTCGCGISTRTVNDNASCRLKQSLCMV 60
Db 180 AAYRLEDTFGDPTMIRANCLVOTTEWSACSKTCGCGISTRTVNDNASCRLKQSLCMV 239
QY 61 RPCEADLEENIKKGKKCIRTPIKSKIPKIFELSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
Db 240 RPCEADLEENIKKGKKCIRTPIKSKIPKIFELSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 299
QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNGPDNDIFESLYRKMYGDMA 170
Db 300 TLPVEFKCPDGEVNMKNMFIKTCACHYNGPDNDIFESLYRKMYGDMA 349

RESULT 2
A40578
beta IG-M2 protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 01-Dec-2000
C:Accession: A40578; A53228
R:Brunner, A.; Chinn, J.; Neubauer, M.; Purchio, A.F.
DNA Cell Biol. 10, 293-300, 1991
A:Title: Identification of a gene family regulated by transforming growth factor-beta
A:Reference number: A40578; MUID:91229699

Tue Aug 21 08:16:54 2001

gene novH protein - human
 C:Species: Homo sapiens (man)
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 05-Nov-1999
 C:Accession: I38069
 R:Martinierie, C.; Huff, V.; Joubert, I.; Badzioch, M.; Saunders, G.; Strong, L.; Perb
 Oncogene 9, 2729-2732, 1994
 A:Title: Structural analysis of the human nov proto-oncogene and expression in Wilms
 Cell Growth Differ. 2, 225-233, 1991
 A:Reference number: I38069; MUID:94336229
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-357 <RES>
 A:Cross-references: EMBL:X78351; NID:g587422; PIDN:CAA55146.1; PID:g825696
 C:Genetics:
 A:Gene: novH
 A:Introns: 28/3; 104/1; 188/1; 259/3
 C:Superfamily: thrombospondin type 1 repeat homology
 F:203-250/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 97.7%; Score 926; DB 2; Length 348;
 Best Local Similarity 95.9%; Pred. No. 1.2e-73;
 Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAYRLEDFGDPPTMIRANCLVQTTEWSACSKTCGCGISTRTVNDNASCRLEKQSRCLMW 60
 DB 179 AAYRLEDFGDPPTMIRANCLVQTTEWSACSKTCGCGISTRTVNDNASCRLEKQSRCLMW 238
 QY 61 RPEADLEENIKKKKCIKTRPKISKPIKIFELSGCTSMKTYRAKFCGCTDGRCTPHRTT 120
 DB 239 RPEADLEENIKKKKCIKTRPKIAKPVKIFELSGCTSVKTYRAKFCGCTDGRCTPHRTT 298
 QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCGNDIFESLYRKMVGDM 170
 DB 299 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCGNDIFESLYRKMVGDM 348

RESULT 3
 S20078
 NOV protein - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S20078
 R:Joliot, V.; Martinierie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, J.; Perb
 Mol. Cell. Biol. 12, 10-21, 1992
 A:Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in myel
 A:Reference number: S20078; MUID:92107157
 A:Accession: S20078
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-351 <JOL>
 A:Cross-references: EMBL:X59284; NID:g63702; PIDN:CAA41975.1; PID:g63703
 C:Genetics:
 A:Gene: NOV

Query Match 57.0%; Score 540.5; DB 2; Length 351;
 Best Local Similarity 59.9%; Pred. No. 5.4e-40;
 Matches 94; Conservative 22; Mismatches 40; Indels 1; Gaps 1;
 QY 1 AAYRLEDFGDPPTMIRANCLVQTTEWSACSKTCGCGISTRTVNDNASCRLEKQSRCLMW 60
 DB 183 AAYRLEATLGIDVSDSSANCIEQTEWASCKSCGCGFSTRTVNRNOCCEMLKOTRLCMV 242
 QY 61 RPEADLEENIKKKKCIKTRPKISKPIKIFELSGCTSMKTYRAKFCGCTDGRCTPHRTT 120
 DB 243 RPEADLEENIKKKKCIKTRPKIAKPVKIFELSGCTSVKTYRAKFCGCTDGRCTPHRTT 301
 QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCGNDIF 157
 DB 302 TIQVEFRCPQGGFLKPKPMMLINTVCVCHGNCPOSNAF 338

RESULT 4
 I38069
 NOV protein - human
 C:Species: Homo sapiens (man)
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 05-Nov-1999
 C:Accession: I38069
 R:Martinierie, C.; Huff, V.; Joubert, I.; Badzioch, M.; Saunders, G.; Strong, L.; Perb
 Oncogene 9, 2729-2732, 1994
 A:Title: Structural analysis of the human nov proto-oncogene and expression in Wilms
 Cell Growth Differ. 2, 225-233, 1991
 A:Reference number: I38069; MUID:94336229
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-357 <RES>
 A:Cross-references: EMBL:X78351; NID:g587422; PIDN:CAA55146.1; PID:g825696
 C:Genetics:
 A:Gene: novH
 A:Introns: 28/3; 104/1; 188/1; 259/3
 C:Superfamily: thrombospondin type 1 repeat homology
 F:203-250/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 54.3%; Score 515; DB 2; Length 357;
 Best Local Similarity 54.4%; Pred. No. 9.2e-38;
 Matches 93; Conservative 25; Mismatches 51; Indels 2; Gaps 2;
 QY 1 AAYRLEDFGDPPTMIRANCLVQTTEWSACSKTCGCGISTRTVNDNASCRLEKQSRCLMW 60
 DB 187 AAYRLEATLGVEVSDSSVNCIEQTEWASCKSCGCGFSTRTVNRNOCCEMLKOTRLCMV 246
 QY 61 RPEADLEENIKKKKCIKTRPKISKPIKIFELSGCTSMKTYRAKFCGCTDGRCTPHRTT 119
 DB 247 RPEADLEENIKKKKCIKTRPKIAKPVKIFELSGCTSVKTYRAKFCGCTDGRCTPHRTT 306
 QY 120 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCGNDIFESLYRKMVGDM 169
 DB 307 KITOAEFQCGQIVKPKVMVIGTCTCHTNCPCKNNEAFLOLELELKTTRGKM 357

RESULT 5
 A35669
 gene CYR61 protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 05-Nov-1999
 C:Accession: A35669; I48319; S16446
 R:O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F.
 Mol. Cell. Biol. 10, 3569-3577, 1990
 A:Title: Expression of cyr61, a growth factor-inducible immediate-early gene.
 A:Reference number: A35669; MUID:90287146
 A:Accession: A35669
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-379 <OAB>
 A:Cross-references: GB:M32490; NID:g192909; PIDN:AAA37512.1; PID:g309206
 A:Note: the authors translated the codon GAT for residue 337 as Gln
 R:Latinkic, B.V.; O'Brien, T.P.; Lau, L.F.
 Nucleic Acids Res. 19, 3261-3267, 1991
 A:Title: Promoter function and structure of the growth factor-inducible immediate ear
 A:Reference number: I48319; MUID:91288203
 A:Accession: I48319
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-379 <RES>
 A:Cross-references: EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g50633
 A:Note: the authors did not translate the codon for residue 108
 A:Note: the authors translated the codon GAT for residue 337 as Gln
 C:Genetics:
 A:Gene: CYR61
 A:Introns: 21/3; 93/1; 208/1; 279/3
 C:Superfamily: von Willebrand factor type C repeat homology
 F:99-166/Domain: von Willebrand factor type C repeat homology <WVC>

Query Match 51.4%; Score 487.5; DB 2; Length 379;
 Best Local Similarity 49.4%; Pred. No. 2.4e-35;

C:Genetics:
A:Gene: CESP:F25H8.3
A:Map position: 4
A:Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1;

Query Match 12.2%; Score 116; DB 2; Length 2165;
Best Local Similarity 21.3%; Pred. No. 0.031;
Matches 50; Conservative 31; Mismatches 52; Indels 102; Gaps 14;

QY 13 PTMIR---ANCLVQT- -EWSACS KTCG MGISPRVT-----NDNAS----- 48
 ||| || | : || : : ||||:|| : || : || : || :
DB 1798 PTSIRECDTSCNP YEWPGDQMOTCSKSGEGVQTRVCRRKNFNS TIPIIFMLEDEPA 1857

QY 49 -----CRL-----EKOSR LCMVRPCEADLE-----ENIKKGK-KCIPTPKISK 85
 | | : : || : : || :
DB 1858 VPKECELFPKP NESQTCELNPCDS EFKWSPGWGEC SKNGCGIGIRRRVKCV----AND 1913

QY 86 PIKFELSGCTSMKYTKRAKFGVGVTDGRCCRP----- 116
 : | || : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1914 GRRYERVKCTTKPPRTQYC--- -FERNC LPSTQEQLSKNQNKAKDGNY TILLDGFTEI 1969

QY 117 --HR-TTLTP-----VEFKCPDGVMKKNMFIKTC-----ACHYN CGDNMD 155
 || : || : || : || : || : || : || : || : || : || : || : || : || : || :
DB 1970 YCHRN MSTIPRAYLNVAP RTNFAEVYGKKLIYPHTCFPFNGDRNDSCH-- -CSEDGD 2022

RESULT 8
T18856
angiogenesis inhibitor homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18856; T24653
R:McMurray, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19031
A:Accession: T18856
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1444 <WL>
A:Cross-references: EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1
A:Experimental source: clone C02B4
R:McMurray, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19917
A:Accession: T24653
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1444 <WI2>
A:Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
A:Experimental source: clone T07C5
C:Genetics:
A:Gene: CESP:C02B4.1
A:Map position: X
A:Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3;

Query Match 11.3%; Score 107; DB 2; Length 1444;
Best Local Similarity 26.1%; Pred. No. 0.13;
Matches 29; Conservative 15; Mismatches 45; Indels 22; Gaps 3;

QY 25 TEWSACSKTCGM-GISTR- -VTNDNASCRLEKSR LCMVRPCEADLE ENIKKGKCIRT 80
 ::||:||||:||||| ||| ||| :|| : || : || : || : || : || : || : || : || : || :
DB 1072 SDWSCSKSCQGDI QTFQKLCLFNNAECSSYAERCKDLPSCSSISSORTTISENGFDA 1131

QY 81 PKISKPIKFELSGCTSMKYTKRAFCGV-----CTDGR C 113
 | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1132 PRWSEWSWSACSFSLTSTRRRRCQQVPDTVGFCAGATILEIQIPCAGGC 1182

RESULT 9
T18397
protein CTRP - malaria parasite (Plasmodium falciparum)

```

A:Accession: A47723
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-803 <RUI>
A:Cross-references: GB:L09123; NID:g409244; PID:g409245
A:Superfamily: F-spondin; thrombospondin type 1 repeat homology
F:435-489/Domain: thrombospondin type 1 repeat homology <THR1>
F:607-662/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match      10.4%  Score 99;  DB 2;  Length 803;
Best Local Similarity 26.8%  Pred. No. 0.39;
Matches 38;  Conservative 64;  Indels 22;  Gaps 6;

OV      21  LVQTTWSACSKTCGMG--ISTRVTN-----DNASCRLEKQSRCLCMVRPCE---ADLEEN 70

```


Search completed: August 20, 2001, 22:53:13
Job time: 588 sec

GenCore_version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2001, 22:47:55 ; Search time 57.66 Seconds
(without alignments)
100.996 Million cell updates/sec

Title: US-09-461-646-2_COPY_180_349

Perfect score: 948

Sequence: 1 AYRLIEDFGDPTMIRANCR.....PCGDNDFESLYRKYMGDMA 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	948	100.0	349	1	CTGF_HUMAN
2	929	98.0	349	1	CTGF_PIG
3	926	97.7	348	1	CTGF_MOUSE
4	906	95.6	349	1	CTGF_BOVIN
5	541.5	57.1	353	1	NOV_CORJA
6	540.5	57.0	351	1	NOV_CHICK
7	518.5	54.7	343	1	NOV_XENLA
8	515	54.3	357	1	NOV_HUMAN
9	512.5	54.1	354	1	NOV_MOUSE
10	487.5	51.4	379	1	CYR6_MOUSE
11	485.5	51.2	381	1	CYR6_HUMAN
12	479.5	50.6	375	1	CE10_CHICK
13	101.5	10.7	465	1	NRTX_CHICK
14	101.5	10.7	807	1	FSPO_RAT
15	99	10.4	803	1	FSPO_XENLA
16	97	10.2	4753	1	LRP_CAEEL
17	94	9.9	463	1	NRTX_MOUSE
18	94	9.9	464	1	NRTX_HUMAN
19	92	9.7	1205	1	ATS2_BOVIN
20	89.5	9.4	388	1	CSP_PLARE
21	89.5	9.4	1178	1	TSP2_CHICK
22	89	9.4	1173	1	TSP1_XENLA
23	88.5	9.3	105	1	MT1_TETPI
24	88.5	9.3	464	1	GDNR_HUMAN
25	88.5	9.3	469	1	GDNR_CHICK
26	88.5	9.3	810	1	NELL_HUMAN
27	87.5	9.2	412	1	CSP_PLAFA
28	87.5	9.2	424	1	CSP_PLAFW
29	87.5	9.2	442	1	CSP_PLAFW
30	87.5	9.2	1211	1	ATS2_HUMAN
31	87	9.2	732	1	2267_HUMAN
32	87	9.2	837	1	MUCL_RAT
33	87	9.2	1170	1	TSPI_HUMAN

34	86	9.1	1170	1	TSPI_BOVIN
35	86	9.1	1170	1	TSPI_MOUSE
36	85	9.0	151	1	KR2C_SHEEP
37	84.5	8.9	397	1	CSP_PLAFO
38	84	8.9	1170	1	TSPI_BOVIN
39	84	8.9	2146	1	INSR_DROME
40	83.5	8.8	810	1	NELL_RAT
41	83.5	8.8	1584	1	BAIL_HUMAN
42	82.5	8.7	934	1	CO6_HUMAN
43	82	8.6	4289	1	TENX_HUMAN
44	81.5	8.6	4655	1	LRP2_HUMAN
45	81	8.5	610	1	TOH2_CAEEL

ALIGNMENTS

RESULT 1	
CTGF_HUMAN	
ID CTGF_HUMAN STANDARD; PRT; 349 AA.	
AC P29279;	
DT 01-DEC-1992 (Rel. 24, Created)	
DT 01-DEC-1992 (Rel. 24, Last sequence update)	
DT 01-OCT-2000 (Rel. 40, Last annotation update)	
DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.	
GN CTGF.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE-Umbilical vein endothelial cells;	
RX MEDLINE=91373462; PubMed=1654338;	
RA Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.;	
RT "Connective tissue growth factor: a cysteine-rich mitogen secreted by	
RT human vascular endothelial cells is related to the SRC-induced	
RT immediate early gene product CEF-10.";	
RL J. Cell Biol. 114:1285-1294(1991).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC TISSUE-Umbilical vein endothelial cells;	
RX MEDLINE=93187114; PubMed=1293144;	
RA Igarashi A., Bradham D.M., Okochi H., Grotendorst G.R.;	
RT "Connective tissue growth factor.";	
RL J. Dermatol. 19:642-643(1992).	
RN [3]	
RP SEQUENCE FROM N.A.	
RC MEDLINE=97207446; PubMed=9054739;	
RA Omar B.S., Werner A., Garnier J.M., Do D.D., Godoy N., Nauck M.,	
RA Marz W., Rupp J., Pech M., Luescher T.F.;	
RT "Human connective tissue growth factor is expressed in advanced	
RT atherosclerotic lesions.";	
RL Circulation 95:831-839(1997).	
CC -!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY	
CC HUMAN VASCULAR ENDOTHELIAL CELLS. THIS IMMEDIATE-EARLY PROTEIN	
CC MAY BIND ONE OF THE PDGF CELL SURFACE RECEPTORS.	
CC -!- SUBUNIT: MONOMER.	
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A	
CC SHORT FORM; SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.	
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING	
CC PROTEIN FAMILY. CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.	
CC -!- SIMILARITY: CONTAINS 1 WVFC DOMAIN.	
CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).	
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CC or send an email to license@isb-sib.ch).	
CC -----	

CTGF. Sus scrofa (Pig).
 NCBI_TaxID=9823;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Uterus;
 MEDLINE=97390475; PubMed=9242708;
 Briggstock D.R., Steffen C.U., Kim G.Y., Vegunta R.K., Diehl J.R.,
 Harding P.A.;
 "Purification and characterization of novel heparin-binding growth
 factors in uterine secretory fluids. Identification as heparin-
 regulated Mr 10,000 forms of connective tissue growth factor.";
 J Biol Chem. 272:20275-20282(1997).

Tue Aug 21 08:16:55 2001

1;

Matches 94; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

Db 180 AAYRLEDTPDPTMTIRANCVQVTTWESAKYKTCGNGISTRTVNDNACFRLKQSRCLCMV 239
QY 61 RPEADLEENIKGKKCIKTPKISPIKELSGCTSMKTYRAKFCGVCCTDGRCCCTPHRTT 120
Db 240 RPEADLEENIKGKKCIKTPKISPIKELSGCTSMKTYRAKFCGVCCTDGRCCCTPHRTT 299
QY 121 TLPVEFKCPDGEVYKNNMFIKTCACHYKNCPGDNDIFESLYYKMYGDMA 170
Db 300 TLPVEFKCPDGEVYKNNMFIKTCACHYKNCPGDNDIFESLYYKMYGDMA 349

RESULT 5
NOV_COTJA STANDARD; PRT; 353 AA.
ID NOV_COTJA
AC P42642;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE NOV PROTEIN PRECURSOR.
GN NOV.

OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]

RP SEQUENCE FROM N.A.
RA Weiskirchen R., Bister K.; to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
CC GROWTH REGULATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 WFEC DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).

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CC or send an email to license@isb-sib.ch).
CC -----

CC EMBL; U13063; AAA21128.1; -
CC InterPro: IPR000359; -
CC InterPro: IPR000867; -
CC InterPro: IPR000884; -
CC InterPro: IPR001007; -
CC Pfam; PF000007; Cys_knot; 1.
CC Pfam; PF00219; IGFBP; 1.
CC Pfam; PF00090; tsp_1; 1.
CC Pfam; PF00093; vwc; 1.
CC PROSITE; PS00222; IGF_BINDING; 1.
CC PROSITE; PS01185; CTCK_1; 1.
CC PROSITE; PS01225; CTCK_2; 1.
CC PROSITE; PS01208; WFEC; 1.
CC PROTO-oncogene; Growth factor binding; Signal.
CC SIGNAL 1 26
CC CHAIN 27 353
CC DOMAIN 106 172
CC DOMAIN 260 334
CC DISULFID 260 297
CC DISULFID 277 311
CC DISULFID 288 327
CC DISULFID 291 329
CC DISULFID 296 333
CC CARBOHYD 276 276
CC SEQUENCE 353 AA; 38667 MW; 717D9F8533882E89 CRC64;
FT SIGNAL 1 26
FT CHAIN 27 353
FT DOMAIN 106 172
FT DOMAIN 260 334
FT DISULFID 260 297
FT DISULFID 277 311
FT DISULFID 288 327
FT DISULFID 291 329
FT DISULFID 296 333
FT CARBOHYD 276 276
FT SEQUENCE 353 AA; 38667 MW; 717D9F8533882E89 CRC64;

Query Match 57.1%; Score 541.5; DB 1; Length 353;
Best Local Similarity 59.9%; Pred. No. 1.8e-41;

RESULT 6

NOV_CHICK

ID NOV_CHICK

AC P28686;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE NOV PROTEIN PRECURSOR.

GN NOV.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BROWN LEHORN;

RX MEDLINE=92107157; PubMed=1309586;

RA Joliet V., Martinerie C., Dambrine G., Plassiart G., Brisac M.,

Crochet J., Perbal B.;

RT "proliferation rearrangements and overexpression of a new cellular gene

(nov) in myeloblastosis-associated virus type 1-induced

nephroblastomas.";

RL Mol. Cell. Biol. 12:10-21(1992).

CC -!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL

GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WITH

TUMORIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED VERSION

OF NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEF) IS SUFFICIENT

TO INDUCE THE TRANSFORMATION OF CEF IN VITRO.

CC -!- TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN

MUSCLE AND INTESTINE, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN AND

SPLEEN, IN ADULT CHICKEN.

CC -!- DEVELOPMENTAL STAGE: MAVI-INDUCED NEPHROBLASTOMAS EXPRESS A HIGH

LEVEL OF NOV GENE WHOSE TRANSCRIPTION IS NORMALLY ARRESTED IN

ADULT KIDNEY.

CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING

PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.

CC -!- SIMILARITY: CONTAINS 1 WFEC DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).

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or send an email to license@isb-sib.ch).

CC EMBL; X59284; CAA41975.1; -

CC PIR; S20078; S20078.

CC InterPro: IPR000359; -

CC InterPro: IPR000867; -

CC InterPro: IPR000884; -

CC InterPro: IPR001007; -

CC Pfam; PF000007; Cys_knot; 1.

CC Pfam; PF00219; IGFBP; 1.

CC Pfam; PF00090; tsp_1; 1.

CC Pfam; PF00093; vwc; 1.

DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01208; VWFC; 1.
KW Proto-oncogene; Growth factor binding; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 1 351 NOV PROTEIN.
FT DOMAIN 104 170 VWFC.
FT DOMAIN 258 332 CTCK.
FT DISULFID 258 295 BY SIMILARITY.
FT DISULFID 275 309 BY SIMILARITY.
FT DISULFID 286 325 BY SIMILARITY.
FT DISULFID 289 327 BY SIMILARITY.
FT DISULFID 294 331 BY SIMILARITY.
FT CARBOHYD 274 274 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 351 AA; 38268 MW; 1ECB3FA3058C6797 CRC64;

Query Match 57.0%; Score 540.5; DB 1; Length 351;
Best Local Similarity 59.9%; Pred. No. 2.3e-41;
Matches 94; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

Qy 1 AAYRLETFGDPDMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRLCMV 60
Db 183 AAYRQETATLGDVSDSSANCIETQTEWSACSKCGMGFSTRVTRNRNOCCEVMKQTRLCMV 242
Qy 61 RPEADLEENIKKKKCIPTKISKPIKFKELSGCTSMKTYRAKFCGVCCTDRCCTPHRTT 120
Db 243 RPECNE-EPSSDKGKKCIQTKSKMKAVFEYKNTSVQTYPRYCGLCNDRGCTCPHTK 301
Qy 121 TLPVEFKCPDGEVKNMFKTKCACHYNCPGDNDF 157
Db 302 TIQVEFRCPQCKFLKPKMLINTCVCHGNCPSQNNAF 338

RESULT 7
NOV_XENLA
ID NOV_XENLA STANDARD; PRT; 343 AA.
AC P51609;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE NOV PROTEIN HOMOLOG PRECURSOR (XNOV).
GN NOV.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257227; PubMed=8666280;
RA Ying 2., King M.L.;
RT "Isolation and characterization of xnov, a Xenopus laevis ortholog of
RL the chicken nov gene.";
RL Gene 171:243-248(1996).
CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
CC GROWTH REGULATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U37063; AAB17096.1; -
DR InterPro; IPR000359; -.

DR InterPro; IPR000867; -
DR InterPro; IPR000884; -
DR InterPro; IPR001007; -
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; vwc; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS01208; VWFC; 1.
DR PROSITE; PS01185; CTCK_1; FALSE_NEG.
DR PROSITE; PS01225; CTCK_2; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 1 343 NOV PROTEIN HOMOLOG.
FT DOMAIN 93 159 VWFC.
FT DOMAIN 249 323 CTCK.
FT DISULFID 249 286 BY SIMILARITY.
FT DISULFID 266 300 BY SIMILARITY.
FT DISULFID 277 316 BY SIMILARITY.
FT DISULFID 280 318 BY SIMILARITY.
FT DISULFID 285 322 BY SIMILARITY.
FT CARBOHYD 265 265 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 343 AA; 38070 MW; 677D7078EB21365F CRC64;

Query Match 54.7%; Score 518.5; DB 1; Length 343;
Best Local Similarity 57.2%; Pred. No. 2e-39;
Matches 91; Conservative 22; Mismatches 45; Indels 1; Gaps 1;

Qy 1 AAYRLETFGDPDMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRLCMV 60
Db 172 AAYRPEATLGDASDTSPACIAQTSTENSACSKTCGMGVSSRTVTRNRNARCEMQKQIRLCMV 231
Qy 61 RPEADLEENI-KKKKCIPTKISKPIKFKELSGCTSMKTYRAKFCGVCCTDRCCTPHRT 119
Db 232 RSCBEEPGHVEKKKCKVRVTKTKPIHFYKNTSVQTYPRYCGLCNDRGCTCPHST 291
Qy 120 TLPVEFKCPDGEVKNMFKTKCACHYNCPGDNDF 158
Db 292 KTMHVEFVCPQKRVKPKVMVISTCVCHYNCQDSSLLQ 330

RESULT 8
NOV_HUMAN
ID NOV_HUMAN STANDARD; PRT; 357 AA.
AC P48745;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
GN NOV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=94336229; PubMed=7520150;
RA Martinerie C., Huff V., Joubert I., Badzioch M., Saunders G.,
RA Strong L., Perbal B.;
RT "Structural analysis of the human nov proto-oncogene and expression
RT in Wilms tumor".
RL Oncogene 9:2729-2732(1994).
CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
CC GROWTH REGULATION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: INCREASED EXPRESSION IN WILMS TUMOR OF THE
CC STROMAL TYPE.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
CC

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AC	P19336;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	01-OCT-1996 (Rel. 34, Last annotation update)
DE	CEF-10 PROTEIN PRECURSOR.
OS	Gallus gallus (Chicken).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89145206; PubMed=2537491;
RA	Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;
RT	"Identification of a phorbol ester-repressible v-src-inducible gene."

RESULT	13
NRTR_CHICK	
ID	NRTR_CHICK
	STANDARD;
	PRT; 465 AA.
AC	O13157;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	01-NOV-1997 (Rel. 37, Last annotation update)
DE	15-DEC-1998 (Rel. 37, Last annotation update)
DE	NEURUTIN RECEPTOR ALPHA PRECURSOR (NTNR-ALPHA)
DE	RECEPTOR BETA) (GDNFR-BETA).
GN	GFR2 OR GDNFRB
OS	Gallus gallus (chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
OC	Archosauria; Aves; Neognathae; Galliformes; Columbiformes
OC	Gallus.

OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97336104; PubMed=9192899;
 RA Rosenthal A., Adu J., Pilon L.G.P., Horton A., Thompson J.,
 RA Bujo-Bello A., Chinchetru M., Buchman V.I., Davies A.M.;
 RA "Neurturin responsiveness requires a GPI-linked receptor and the Ret
 RT receptor tyrosine kinase.";
 RL Nature 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 CC TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 CC RECEPTOR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
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 CC -----
 DR EMBL; U90542; AAB61571.1; -;
 DR Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 KW SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 445 NEURTURIN RECEPTOR ALPHA.
 FT PROPEP 446 465 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 445 445 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 465 AA; 51908 MW; 22CD9024ED971F06 CRC64;

 Query Match 10.7%; Score 101.5; DB 1; Length 465;
 Best Local Similarity 25.8%; Pred. No. 0.039;
 Matches 47; Conservative 15; Mismatches 61; Indels 59; Gaps 12;
 QY 4 RLEDTF-----GPDPT-MIRAN-CLVQTEWSACSKTCGMGISTRVNDNASCRLEQ 54
 DB 134 RLSDIFRLASIFSGMDPATNSKSHCL-----DAAKACNL-----NDNC-----KR 174
 QY 55 SRLCMVRPCADLEENIKKGGKCIPTKISKPIKFSLGCTSMKTYRAKFCGVCTDGRCC 114
 DB 175 LRSQYISTC-----SKEISATEHCSSRR-KCHKALRQFDNVPSEYTYRLFLCS-CKDQACA 228
 QY 115 TPHTTTLPLVEFKCPDGEVAKKNNM-----PIKTCACHY-----NCPG 152
 DB 229 EPRQTIQVFP---CSYEDKEKPNCLDLRNVCRAHLCRSRLADFHANCQASFSQILSCPG 285
 QY 153 DN 154
 DB 286 DN 287
 RESULT 14
 FSPO_RAT STANDARD; PRT; 807 AA.
 ID FSPO_RAT
 AC P35446;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE F-SPONDIN PRECURSOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC. TISSUE=Embryonic floor plate;
 RX MEDLINE=92208952; PubMed=1555244;
 RA Kiar A., Baldassare M., Jessell T.M.;
 RT "F-spondin: a gene expressed at high levels in the floor plate
 RT encodes a secreted protein that promotes neural cell adhesion and
 RT neurite extension.";
 RL Cell 69:95-110(1992).
 CC -1- FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY
 CC NEURON CELLS AND THE OUTGROWTH OF NEURITES IN VITRO. MAY
 CC CONTRIBUTE TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL
 CC CORD AND THE PNS.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE FLOOR PLATE.
 CC -1- SIMILARITY: CONTAINS 6 TYPE-1 TSP DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; M88469; AAA41174.1; -;
 DR PIR; A38152; A38152.
 DR InterPro; IPR000884; -;
 DR InterPro; IPR002861; -;
 DR Pfam; PF02014; Reeler; 1.
 DR Pfam; PF00090; tsp_1; 6.
 DR PROSITE; PS00092; TSP1; 5.
 KW Glycoprotein; Signal; Repeat; Cell adhesion.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 807 F-SPONDIN.
 FT DOMAIN 443 494 TSP TYPE-1 1.
 FT DOMAIN 502 554 TSP TYPE-1 2.
 FT DOMAIN 559 610 TSP TYPE-1 3.
 FT DOMAIN 615 665 TSP TYPE-1 4.
 FT DOMAIN 669 720 TSP TYPE-1 5.
 FT DOMAIN 755 807 TSP TYPE-1 6.
 FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 807 AA; 90773 MW; 309525F9EAFE89A CRC64;

 Query Match 10.7%; Score 101.5; DB 1; Length 807;
 Best Local Similarity 24.7%; Pred. No. 0.065;
 Matches 42; Conservative 19; Mismatches 46; Indels 63; Gaps 10;
 QY 18 ANCLIV-QTTEWSACSKTCGMGISTR-----VTNDNASCRLE-KQSRLCMVRPCE----- 64
 DB 557 SSCLVTWGEWDDCSATCGMGKRRHRVMKSPADGSMCKAETSQAECMMPECHTIPCL 616
 QY 65 -----ADLEENIKKGGKCIPTKISKPIKFSLGCTSMKTYRAKFCGVCTDGRCC 714
 DB 617 LSPWSEWSDCSVTGCGMTRQRMLKSLAELEGDCNEDLEQAEKCM-LPEC--PIDCELS 673
 QY 94 CTSMKTYRAKFCGVCTDGRCCCTPH--RTTTLPLVE-----FKCPDGEVAKK 136
 DB 674 WSQWSECN-KSCG-----KGHMIRTRTIQMEPQFGGAPCPETVQRKK 714
 RESULT 15
 FSPO_XENLA STANDARD; PRT; 803 AA.
 ID FSPO_XENLA
 AC P35447;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE F-SPONDIN PRECURSOR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.

Tue Aug 21 08:16:55 2001

```

OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=93376785; PubMed=8367492;
RX Ruiz I Altaba A.; Cox C.; Jessell T.M.; Klar A.;
RT "Ectopic neural expression of a floor plate marker in frog embryos
RL injected with the midline transcription factor pntallavis.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8268-8272(1993).
CC -1- FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY
CC NEURON CELLS AND THE OUTGROWTH OF NEURITES IN VITRO. MAY
CC CONTRIBUTE TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL
CC CORD AND THE PNS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE FLOOR PLATE.
CC -1- SIMILARITY: CONTAINS 6 TYPE-1 TSP DOMAINS.
CC -----
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CC -----
DR EMBL; L09123; AAA19105.1; -
DR PIR; A47723; A47723.
DR InterPro; IPR000884; -
DR InterPro; IPR002861; -
DR Pfam; PF02014; Reeler; 1.
DR Pfam; PF00090; tsp-1; 6.
DR PROSITE; PS50092; TSP1; 6.
KW Glycoprotein; Signal; Repeat; Cell adhesion.
FT SIGNAL 1 23
FT CHAIN 24 803
FT DOMAIN 437 488 TSP TYPE-1 1.
FT DOMAIN 496 548 TSP TYPE-1 2.
FT DOMAIN 553 604 TSP TYPE-1 3.
FT DOMAIN 609 661 TSP TYPE-1 4.
FT DOMAIN 665 716 TSP TYPE-1 5.
FT DOMAIN 751 803 TSP TYPE-1 6.
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 677 677 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 803 AA; 90702 MW; D3A54E329548AED9 CRC64;

Query Match 10.4%; Score 99; DB 1; Length 803;
Best Local Similarity 26.8%; Pred. No. 0.11;
Matches 38; Conservative 18; Mismatches 64; Indels 22; Gaps 6;

QY 21 LVQTTWNSACSKTCGMG--ISTRTN-----DNASCRLEKOSRLQWVRPCE---ADLEEN 70
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
667 LTEWSYWSSECKNCKGKGMHIRTMTMEPQPGGAVCPETVQRKKCLRKCKKSSGNERH 726
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
71 IKKGKKIRTPKIRKIFELSGCTSMKTYRA-----KFCGVCVDGRCCPTPHRTTLPVE 125
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
727 LKDAKRRRSEKIKEDSDGEQYPVCKMKPWTAWTECTKFCGGIQERFMTVKRKRKSSQF 786
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : :
126 FKCPDGEVNMKNMFIKTCACH 147
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
787 TSCKD----KKE---IRACNVH 801
```

Search completed: August 20, 2001, 22:57:00
Job time: 545 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 20, 2001, 22:46:30 ; Search time 93.5 seconds
(without alignments)
240.555 Million cell updates/sec

Title: US-09-461-646-2_COPY_180_349

Perfect score: 948

Sequence: 1 AAYRLEDFGPDPTMIRANC.....PGDNDFESLYRKMYGDMA 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_16:*

2: sp_archaea:*

3: sp_bacteria:*

4: sp_fungi:*

5: sp_human:*

6: sp_invertebrate:*

7: sp_mammal:*

8: sp_mhc:*

9: sp_organelle:*

10: sp_phase:*

11: sp_plant:*

12: sp_rodent:*

13: sp_unclassified:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	935	98.6	349	6	O97765 sus scrofa
2	930	98.1	349	6	O9GL71 Q9GL71 bos taurus
3	926	97.7	347	11	O9WVS1 Q9WVS1 rattus norv
4	926	97.7	347	11	O9RIE9 Q9RIE9 rattus norv
5	891	94.0	343	13	O42607 Q42607 xenopus lae
6	885	93.4	347	13	O9PT80 Q9PT80 notophthalm
7	566	59.7	113	11	O9Z164 Q9Z164 rattus norv
8	499	52.6	351	11	O9QZQ5 Q9QZQ5 rattus norv
9	489.5	51.6	379	11	O9ES72 Q9ES72 rattus norv
10	487.5	51.4	379	11	O9WTM9 Q9WTM9 rattus norv
11	485.5	51.2	381	4	O43775 O43775 homo sapien
12	423	44.6	367	11	O54775 O54775 mus musculu
13	404	42.6	331	4	O95958 O95958 homo sapien
14	404	42.6	354	4	O95389 O95389 homo sapien
15	402.5	42.5	334	4	O9UID7 O9UID7 homo sapien
16	400.5	42.2	280	4	O9HCS3 O9HCS3 homo sapien
17	400.5	42.2	367	4	O95388 O95388 homo sapien
18	352	37.1	70	13	O9DF21 O9DF21 scylliorhinu
19	236	24.9	128	11	O9R2C0 O9R2C0 rattus norv

20	191	20.1	179	5	O9VVK0 Q9VVK0 drosophila
21	190	20.0	58	6	O97574 O97574 bos taurus
22	148	15.6	250	4	O76076 O76076 homo sapien
23	146	15.4	251	11	Q920G4 Q920G4 mus musculu
24	144	15.2	250	11	Q9JHC6 Q9JHC6 rattus norv
25	123	13.0	100	4	O9UDL6 Q9UDL6 homo sapien
26	116	12.2	2165	5	Q19791 Q19791 caenorhabdi
27	108.5	11.4	1054	5	O9W493 Q9W493 drosophila
28	107	11.3	176	13	O9PSS6 O9PSS6 gallus gall
29	107	11.3	1444	5	Q17591 Q17591 caenorhabdi
30	106.5	11.2	425	6	O02661 O02661 bos taurus
31	105.5	11.1	687	5	Q23729 Q23729 cryptospori
32	102.5	10.8	2098	5	Q25757 Q25757 plasmodium
33	102.5	10.8	2114	5	O97267 O97267 plasmodium
34	101.5	10.7	1235	4	O95428 O95428 homo sapien
35	101	10.7	807	4	O9HCB6 O9HCB6 homo sapien
36	100.5	10.6	808	13	O42113 O42113 brachydanio
37	100.5	10.6	1081	5	O9U631 O9U631 drosophila
38	100.5	10.6	1083	5	O9VTT0 O9VTT0 drosophila
39	99	10.4	712	5	O43981 O43981 eimeria ten
40	98	10.3	769	11	O9QXT7 O9QXT7 mus musculu
41	97	10.2	445	4	O43384 O43384 homo sapien
42	97	10.2	1290	4	Q9UP26 Q9UP26 homo sapien
43	96.5	10.2	432	4	O9NPM2 O9NPM2 homo sapien
44	96.5	10.2	654	5	Q19284 Q19284 caenorhabdi
45	96.5	10.2	898	4	Q9UFZ4 Q9UFZ4 homo sapien

ALIGNMENTS

RESULT 1

ID O97765 PRELIMINARY; PRT; 349 AA.
AC O97765;

DT 01-MAY-1999 (TReMBLrel. 10, Created)

DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)

DE CONNECTIVE TISSUE GROWTH FACTOR.

GN CTGF.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=UTERUS;

RA Harding P.A., Brigstock D.R.;

RT "Cloning and sequencing of a porcine connective tissue growth factor

(CTGF) cDNA";

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U70060; AD00174.1; -

DR InterPro; IPR000359; -

DR InterPro; IPR000867; -

DR InterPro; IPR001007; -

DR Pfam; PF00007; Cys_knot; 1.

DR Pfam; PF00090; tsp_1; 1.

DR Pfam; PF00093; vwc; 1.

DR Pfam; PF00219; IGFBP; 1.

DR PROSITE; PS01185; CTCK_1; 1.

DR PROSITE; PS01225; CTCK_2; 1.

DR PROSITE; PS00222; IGF_BINDING; 1.

DR PROSITE; PS01208; VWFC; 1.

DR SMART; SM00041; CT; 1.

SQ SEQUENCE 349 AA; 37946 MW; 35AB4275AC1D4B3A CRC64;

Query Match 98.6%; Score 935; DB 6; Length 349;

Best Local Similarity 97.6%; Pred. No. 8.2e-93;

Matches 166; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYRLEDFGPDPTMIRANCLVQITWESACSKTCGCGISTRTVNDNASCRLEKQSLRCV 60

RESULT	3
Q9WVS1	PRELIMINARY; PRT; 347 AA.
ID	Q9WS1
AC	Q9WS1;
DT	01-NOV-1999 (TReMBUrel. 12, Created)
DT	01-NOV-1999 (TReMBUrel. 12, Last sequence update)
DT	01-NAR-2001 (TReMBUrel. 16, Last annotation update)
DE	CONNECTIVE TISSUE GROWTH FACTOR.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_Taxid=10116;
RP	[1]
RA	SEQUENCE FROM N.A.
RL	Tezuka K., Tanatani T.;
DR	"Rattus norvegicus connective tissue growth factor." ;
DR	Submitted (FEB-1999) to the EMBL/GenBank/DDSB databases.
DR	EWBL: AB023068; BAA82125.1; -
DR	InterPro: IPR000072; -

```

Query Match          97.7%;   Score 926;   DB 11;   Length 347;
Best Local Similarity 95.9%;   Pred. No. 7.6e-92;
Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

07 79. score 926: dB 11: Length 347;

```
QY 1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMISTRVTNDNASCRLKQSLCMV 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMISTRVTNDNASCRLKQSLCMV 237
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RPEADLEENIKGKKCIKIRPKISKPIKFSLGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 RPEADLEENIKGKKCIKIRPKISKPIKFSLGCTSMKTYRAKFCGCTDGRCCCTPHRTT 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
ID O42607 PRELIMINARY; PRT; 343 AA.
AC O42607;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR XCTGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying Z., King M.L.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U43524; AAB67639.1; -.
DR EMBL; U43523; AAB67638.1; -.
DR InterPro; IPR000359; -.
DR InterPro; IPR000867; -.
DR InterPro; IPR000884; -.
DR InterPro; IPR001007; -.
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; vwc; 1.
DR Pfam; PF00219; IGFBP; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS02022; IGF_BINDING; 1.
DR PROSITE; PS01208; VMFC; UNKNOWN_1.
DR SMART; SM00041; CT; 1.
SQ SEQUENCE 343 AA; 37966 MW; 93F221C5DB565A81 CRC64;

Query Match 94.08; Score 891; DB 13; Length 343;
Best Local Similarity 91.1%; Pred. No. 4.4e-88;
Matches 154; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 2 AYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMISTRVTNDNASCRLKQSLCMVR 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 AFMEETYGDPDSLIRANCLVQTTEWSACSKTCGMISTRVTNDNASCRLKQSLCMVR 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 PCEADLEENIKGKKCIKIRPKISKPIKFSLGCTSMKTYRAKFCGCTDGRCCCTPHRTT 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 PCEADLEENIKGKKCIKIRPKISKPIKFSLGCTSMKTYRAKFCGCTDGRCCCTPHRTT 294
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 LPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 LPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 343
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
ID Q9PT80 PRELIMINARY; PRT; 347 AA.
AC Q9PT80;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR.
```

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GN CTGF.
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;
OC Notophthalmus.
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FORELIMB BLASTEMA;
RA Gates P.B.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-FORELIMB BLASTEMA;
RX MEDLINE=99033008; PubMed=9813273;
RA Cash D.E., Gates P.B., Imokawa Y., Brookes J.P.;
RT "Identification of newt connective tissue growth factor as a target of
retinoid regulation in limb blastema cells.";
RL Gene 222:119-124(1998).
DR EMBL; AJ271167; CAB65965.1; -.
DR InterPro; IPR000359; -.
DR InterPro; IPR000867; -.
DR InterPro; IPR000884; -.
DR InterPro; IPR001007; -.
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; vwc; 1.
DR Pfam; PF00219; IGFBP; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS02022; IGF_BINDING; 1.
DR PROSITE; PS01208; VMFC; UNKNOWN_1.
DR SMART; SM00041; CT; 1.
SQ SEQUENCE 347 AA; 38098 MW; 3B7E2399F27672C1 CRC64;

Query Match 93.4%; Score 885; DB 13; Length 347;
Best Local Similarity 91.2%; Pred. No. 2e-87;
Matches 155; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMISTRVTNDNASCRLKQSLCMV 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 AVYRQEETYGDPDSLIRANCLVQTTEWSACSKTCGMISTRVTNDNASCRLKQSLCMV 237
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RPEADLEENIKGKKCIKIRPKISKPIKFSLGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 RPEADLEENIKGKKCIKIRPKISKPIKFSLGCTSMKTYRAKFCGCTDGRCCCTPHRTT 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
ID Q9Z164 PRELIMINARY; PRT; 113 AA.
AC Q9Z164;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99150373; PubMed=10026205;
RA Murphy M., Godson C., Cannon S., Kato S., Mackenzie H.S., Martin F.,
RA Brady H.R.;
RT "Suppression subtractive hybridization identifies high glucose levels
as a stimulus for expression of connective tissue growth factor and
other genes in human mesangial cells.";
RN [1]
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Tue Aug 21 08:16:55 2001

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J. Biol. Chem. 274:5830-5834(1999).
DR EMBL: AF079531; AAD02838.1; -.
DR InterPro: IPR000359; -.
DR Pfam: PF00007; Cys_knot; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR SMART: SM00041; CT; 1.
FT NON_TER 113
FT SEQUENCE 113 AA; 12767 MW; 23EA69FC0A60635E CRC64;
SQ

Query Match          59.7%; Score 566; DB 11; Length 113;
Best Local Similarity 93.5%; Pred. No. 1.5e-53;
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 38 ISTRVTNDNASCRLEKQSRCLMVRPCADLEENIKKGGKCIPTPKISKPKIFELSGCTSM 97
DB 1 ISTRVTNDNTFCRLKQSRCLMVRPCADLEENIKKGGKCIPTPKIAKPKVFKELSGCTSV 60
QY 98 KTYRAKFCGCTDGRCTPHTTTLPVEFKCPDGEVYMKNNMFIKTCA 145
DB 61 KTYRAKFCGCTDGRCTPHTTTLPVEFKCPDGEVYMKNNMFIKTCA 108

RESULT 8
ID Q9QZQ5 PRELIMINARY; PRT; 351 AA.
AC Q9QZQ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE NOV PROTEIN.
GN NOV.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=2003572; PubMed=10570975;
RA Liu C., Liu X.-J., Crowe P.D., Kellner G.S., Fan J., Barry G., Manu F.,
RA Ling N., De Souza E.B., Maki R.A.;
RT "Nephroblastoma overexpressed gene (NOV) codes for a growth factor
RT that induces protein tyrosine phosphorylation.";
RL Gene 238:471-478(1999).
DR EMBL: AF171936; AAD49371.1; -.
DR InterPro: IPR000359; -.
DR InterPro: IPR000867; -.
DR InterPro: IPR000884; -.
DR InterPro: IPR001007; -.
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00093; vwc; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS01208; WMFC; UNKNOWN_1.
DR SMART: SM00041; CT; 1.
DR SEQUENCE 351 AA; 38509 MW; 02619707DE7C1BFB CRC64;
SQ

Query Match          52.6%; Score 499; DB 11; Length 351;
Best Local Similarity 53.5%; Pred. No. 7.5e-46;
Matches 91; Conservative 26; Mismatches 51; Indels 2; Gaps 2;

QY 2 AYRLDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRCLMVR 61
DB 182 AYRPATVGVLSDDSSINCIBQTTEWSACSKTCGMGLSTRVTRNLCQENKVKQTRCLMVR 241
QY 62 PCEADL-EENTKKKKCIPTPKISKPKIFELSGCTSMKTYRAKFCGCTDGRCTPHTTT 120
DB 113

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242 PCEQEPGEATDMGKKKCLRTKKSILHLOFNKNTSLTYTKPRFCGICSDGRCTPFNTK 301
121 TLPVEFKCPDGEVYMKNNMFIKTCAHYNCPCGNDIF-ESLYYRKMVGDM 169
113
302 TIQVEFOCLPQIIKPKVWIGTCTCHSNCPQNEAFLOELKLTSGEM 351
113

RESULT 9
Q9ES72 PRELIMINARY; PRT; 379 AA.
ID Q9ES72
AC Q9ES72;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYSTEINE-RICH PROTEIN 61.
GN CYR61.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG, AND PLACENTA;
RX MEDLINE=20435857; PubMed=10852911;
RA Albrecht C., von Der Kammer H., Mayhaus M., Klaudiny J., Schweizer M.,
RA Nitsch R.M.;
RT "Muscarinic acetylcholine receptors induce the expression of the
RT immediate early growth regulatory gene CYR61.";
RL J. Biol. Chem. 275:28929-28936(2000).
DR EMBL: AF218568; AAG14964.1; -.
DR SEQUENCE 379 AA; 41687 MW; 62BF0BBA4C5AFDE9 CRC64;
SQ

Query Match          51.6%; Score 489.5; DB 11; Length 379;
Best Local Similarity 49.4%; Pred. No. 8.5e-45;
Matches 83; Conservative 33; Mismatches 43; Indels 9; Gaps 2;

QY 9 FGPDPTMI-----RANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRCLMVR 61
DB 209 FGTEPRVLYNPLHAHGOKCIVQTSQCSKCGTGISTRVNDNSECLRVETREICEVR 268
113
62 PCEADLEENIKKKCIPTPKISKPKIFELSGCTSMKTYRAKFCGCTDGRCTPHTTT 121
113
269 PCGGPVYSSLUKKKKCKSKTKKSPVPVFTYAGSSVKKYKPCGSCVDGRCCTPLOTRT 328
113
122 LPVEFKCPDGEVYMKNNMFIKTCAHYNCPCGNDIFESLYYRKMVGDM 169
113
329 VKMRFCEGDEMFSKNVYMTQSCKCNPCPNPNEASFRLY--SLFNDI 374
113

RESULT 10
Q9WTM9 PRELIMINARY; PRT; 379 AA.
ID Q9WTM9
AC Q9WTM9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYR61 PRECURSOR.
GN CYR61.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IZM; TISSUE=AORTA;
RA Unoki H., Yonekura H., Furukawa K., Yamamoto H.;
RT "Rat Cyr61 mRNA.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB075877; BAA78339.1; -.
DR InterPro: IPR000359; -.
DR InterPro: IPR000867; -.
DR InterPro: IPR000884; -.

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[illegible]

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.Db 215 NCIAVTPSPSCSTCGLGISTRISNVNARCWPEQSRCLNLRPCDVIDIOLHIKAKKCL 274
QY 79 RTPKISPIKIFELSGTSMKTYRAKFCGVCCTGRCCTPHRTTLPVEFKCPDGEVMMKNN 138
Db 275 AVYQPEATNFTLAGCVSTYRKYKCGVCTDNRCCTPIYKSKTISVDFQCPEGPGSRQV 334
QY 139 MFIKTCACHYNGCDNDIFESL 160
Db 335 LWINACFCNLSCRPNDFADL 356

RESULT 13
O95958 PRELIMINARY; PRT; 331 AA.
AC O95958;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE DJ142L7.3 (CONNECTIVE TISSUE GROWTH FACTOR (NOV, GIG) LIKE PROTEIN)
DE (FRAGMENT).
OS Homo sapiens (Human).
GN DJ142L7.3 OR LIBC.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE-BONE MARROW, AND FETAL KIDNEY;
RX MEDLINE=99061933; PubMed=9843955;
RA Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J.,
RA Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen R.L.,
RA Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J.,
RA Gurney A.L., Botstein D., Levine A.J.;
RT "Wisp genes are members of the connective tissue growth factor family
RT that are up-regulated in wnt-1-transformed cells and aberrantly
RT expressed in human colon tumors."
RL Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).
DR EMBL; AF100781; AAC96323.1; -
DR InterPro: IPR000359; -
DR InterPro: IPR000867; -
DR InterPro: IPR000884; -
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00041; CT; 1.
SQ SEQUENCE 354 AA; 39292 MW; 67F48D0D5C2F5EE3 CRC64;

SEQUENCE FROM N.A.
RC TISSUE-MAMMARY GLAND;
RA van Golen K.L., Davies S., Wu Z.F., Wang Y.F., Bucana C.D., Root H.,
RA Chandrasekharappa S., Strawderman M., Ethier S.P., Merajver S.D.;
RT "A novel putative IGF-binding, tumor suppressor protein, LIBC, and
RT rhoC Gpase, are determinants of the inflammatory breast cancer
RT phenotype";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99289; CAB16556.1; -
DR EMBL; AF143679; AAD31517.1; -
DR InterPro: IPR000359; -
DR InterPro: IPR000867; -
DR InterPro: IPR000884; -
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00041; CT; 1.
FT NON_TER 331
SQ SEQUENCE 331 AA; 36909 MW; D109C2FDCA1DF549 CRC64;

Query Match 42.6%; Score 404; DB 4; Length 331;
Best Local Similarity 42.2%; Pred. No. 1.2e-35;
Matches 68; Conservative 37; Mismatches 55; Indels 2; Gaps 1;

QY 2 AYRLDTFGDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMWR 61
Db 168 SYKTMAYRNLPILWKKCLVQATKTPCSTCGMISNRTNENSCMRKRLCYIQ 227
QY 62 PCADLEENIK--KGKKCIPTPKISPIKIFELSGTSMKTYRAKFCGVCCTGRCCTPHRT 119
Db 228 PCDSNLIKTIKIPKGTCTQPTFOLSKRAEKFVFGSCSSTQSYKPTFCGICLDKRCCLPNKS 287
QY 120 TTLPVEFKCPDGEVMMKNNFIKTCACHYNGCDNDIFESL 160
Db 288 KMITIQDCPNEGSKWMLWITSCVCQRCNCRPGDIFSEL 328

RESULT 14
O95389 PRELIMINARY; PRT; 354 AA.
ID O95389
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AC O95389;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR RELATED PROTEIN WISP-3.
GN WISP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW, AND FETAL KIDNEY;
RX MEDLINE=99061933; PubMed=9843955;
RA Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J.,
RA Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen R.L.,
RA Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J.,
RA Gurney A.L., Botstein D., Levine A.J.;
RT "Wisp genes are members of the connective tissue growth factor family
RT that are up-regulated in wnt-1-transformed cells and aberrantly
RT expressed in human colon tumors."
RL Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).
DR EMBL; AF100781; AAC96323.1; -
DR InterPro: IPR000359; -
DR InterPro: IPR000867; -
DR InterPro: IPR000884; -
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00041; CT; 1.
SQ SEQUENCE 354 AA; 39292 MW; 67F48D0D5C2F5EE3 CRC64;

Query Match 42.6%; Score 404; DB 4; Length 354;
Best Local Similarity 42.2%; Pred. No. 1.3e-35;
Matches 68; Conservative 37; Mismatches 54; Indels 2; Gaps 1;

QY 2 AYRLDTFGDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMWR 61
Db 191 SYKTMAYRNLPILWKKCLVQATKTPCSTCGMISNRTNENSCMRKRLCYIQ 250
QY 62 PCADLEENIK--KGKKCIPTPKISPIKIFELSGTSMKTYRAKFCGVCCTGRCCTPHRT 119
Db 251 PCDSNLIKTIKIPKGTCTQPTFOLSKRAEKFVFGSCSSTQSYKPTFCGICLDKRCCLPNKS 310
QY 120 TTLPVEFKCPDGEVMMKNNFIKTCACHYNGCDNDIFESL 160
Db 311 KMITIQDCPNEGSKWMLWITSCVCQRCNCRPGDIFSEL 351

RESULT 15
O95389 PRELIMINARY; PRT; 334 AA.
ID O95389
AC O95389;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CYR61 PROTEIN.
GN CYR61.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 1-107 FROM N.A.
RC TISSUE-KIDNEY;
RA Anding B., Long Y.;
RT "Cloning of a new gene down-regulated in the small-cell tumor
RT embryonal-rhabdomyosarcoma (RMS).";
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF003114; AAF21597.1; -
DR EMBL; AF003114; AAF21597.1; -
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DR InterPro: IPR000359; -
DR InterPro: IPR000867; -
DR InterPro: IPR000884; -
DR InterPro: IPR001007; -
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00093; wsc; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS01208; VWFC; 1.
DR SMART: SM00041; CT; 1.
SQ SEQUENCE 334 AA; 37246 MW; 9188987A7352E948 CRC64;

Query Match 42.5%; Score 402.5; DB 4; Length 334;
Best Local Similarity 45.7%; Pred. No. 1.8e-35;
Matches 79; Conservative 26; Mismatches 47; Indels 21; Gaps 6;

Qy 9 FGPDPTMIRAN-----CLVOTTEWSAGSKTCGGMGISTRTVNDNASCRLEKQSLCMYRP 62
   || : || | | : || || || || || || || || || || || || || || || || ||
Db 166 FGMEP-RIRYNPLOGQKCIIVOTTSWSQCSKTCGTGISTRTVNDNPECRLEKTRICEVRP 224
   | : : : || || || : | : || : | : || : | : || || || || || || || ||
Qy 63 CEADLEENIKKGKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCTDGRCTPHRTTTL 122
   | : : : || || || : | : || : | : || : | : || || || || || || || ||
Db 225 CGQVYSSLRKKGKSKTKSPVRFYTAGCLSVKRYRPKYCGSCVDGRCTPOLTRT- 283
   | : : : | : | : | : || || | : || || | : || || | : || || | : || ||
Qy 123 PVEFKCPDGEVMKK-NMFIK-----TCACHYNPCGNDIFESLYYRKMVGDM 169
   | : : : | : | : | : || || | : || || | : || || | : || || | : || ||
Db 284 -----CEDAVPLRRWGDIFQERHDDPVLKCNYNCPHANEAAFPFY--RLFNDI 329
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Search completed: August 20, 2001, 22:55:51
Job time: 561 sec

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